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Fig. 1

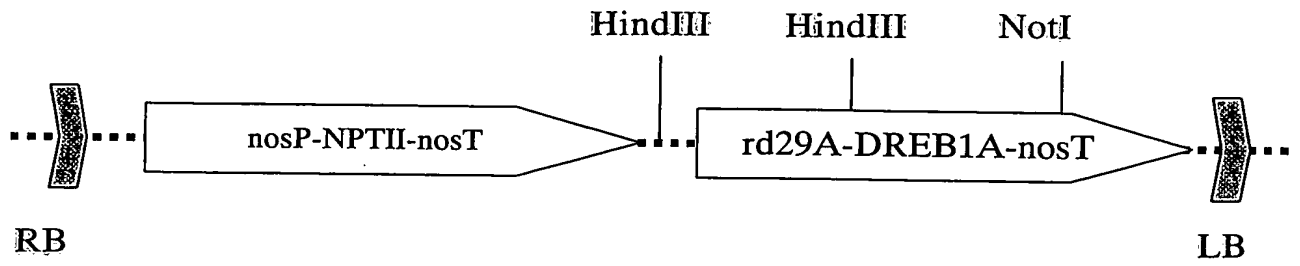


Fig. 2-1

0009114

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Sequence 1 : DREB1A.nuc
 Size : 651
 Matching Position : 1 - 651

Sequence 2 : DREB1B.nuc
 Size : 642
 Matching Position : 1 - 642

Matching Condition.

Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2

Matching : 85.04 [%]
 Weight : -451

```

1 : ATGAAGTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTCC
   ***** **
1 : ATGAAGTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAG-- -----CC

61 : TC-AGGCGGT GATTATATTC CGACGCTTGC GAGCAGCTGC CCCAAGAAAC CGGCGGGTCG
   ** ***** **
51 : TCAAGGCGGA GATTATTGTC CGACGTTGGC CACGAGTTGT CCGAAGAAAC CGGCGGGCCG

120 : TAAGAAGTTT CGTGAGACTC GTCACCCAAT ATACAGAGGA GTTCGTCGGA GAAACTCCGG
   *****
111 : TAAGAAGTTT CGTGAGACTC GTCACCCAAT TTACAGAGGA GTTCGTCAAA GAAACTCCGG

180 : TAAGTGGGTT TGTGAGGTTA GAGAACCAAA CAAGAAAACA AGGATTTGGC TCGGAACATT
   ***** *
171 : TAAGTGGGTT TCTGAAGTGA GAGAGCCAAA CAAGAAAACC AGGATTTGGC TCGGGACTTT

240 : TCAAACCGCT GAGATGGCAG CTCGAGCTCA CGACGTTGCC GCTTTAGCCC TTCGTGGCCG
   *****
231 : CCAAACCGCT GAGATGGCAG CTCGAGCTCA CGACGTCGCT GCATTAGCCC TCCGTGGCCG

300 : ATCAGCCTGT CTCAATTTTCG CTGACTCGGC TTGGAGACTC CGAATCCCGG AATCAACTTG
   *****
291 : ATCAGCATGT CTCAACTTTCG CTGACTCGGC TTGGCGGCTA CGAATCCCGG AGTCAACATG

360 : CGCTAAGGAC ATCCAAAAGG CGGCGGCTGA AGCTGCGTTG GCGTTTCAGG ATGAGATGTG
   ***
351 : CGCCAAGGAT ATCCAAAAGG CGGCTGCTGA AGCGGCGTTG GCTTTTCAAG ATGAGACGTG

420 : TGATGCGACG ---ACGGATC ATGGCTTCGA CATGGAGGAG ACGTTGGTGG AGGCTATTTA
   ****
411 : TGATACGACG ACCACGAATC ATGGCTTCGA CATGGAGGAG ACGATGGTGG AAGCTATTTA

477 : CACGCGGAA CAGAGCGAAA ATGCGTTTTA TATGCAGAT GAGCGATGT TTGAGATGCC
   **
471 : TACACGGAA CAGAGCGAAG GTGCGTTTTA TATGATGAG GAGACAATGT TTGGATGCC

537 : GAGTTTGTG GCTAATATGG CAGAAGGGAT GCTTTTGCCG CTTCGTCGG TACAGTGAA
   **
531 : GACTTTGTG GATAATATGG CTGAAGGCAT GCTTTTACCG CCGCGTCTG TTCAATGAA

597 : TCATAATCAT GAAGTCGACG GCGATGATGA CGACGTATCG TTATGGAGTT ATTAA
   *****

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Fig. 2-2

0009114

591 : TCATAATTAT GACGGCGAAG GAGATGGT-- -GACGTGTCG CTTTGGAGTT ACTAA

+++++

Sequence 1 : DREB1A.nuc
Size : 651
Matching Position : 1 - 651

Sequence 2 : DREB1C.nuc
Size : 651
Matching Position : 1 - 651

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 86.70 [%]
Weight : -476

1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTCC
***** ** *****
1 : ATGAACTCAT TTTCTGCCTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTCC

61 : TCAGGCGGTG ATTATATTCC GACGCTTGGC AGCAGCTGCC CCAAGAAACC GGCGGGTCGT
***** ** * ** * ***** * *****
61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATA TACAGAGGAG TTCGTGGGAG AAACCTCCGGT
***** ***** ***** ***** ***** ** *****
121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAACCTCCGGT

181 : AAGTGGGTTT GTGAGGTTAG AGAACCAAAC AAGAAAACAA GGATTGGCT CGGAACATT
***** * ***** * ** * ***** * *****
181 : AAGTGGGTGT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGATTGGCT CGGGACTTTC

241 : CAAACCGCTG AGATGGCAGC TCGAGCTCAC GACGTTGCCG CTTTAGCCCT TCGTGGCCGA
***** ***** *** ***** ***** * *****
241 : CAAACCGCTG AGATGGCAGC TCGTGCTCAC GACGTCGCCG CCATAGCTCT CCGTGGCAGA

301 : TCAGCCTGTC TCAATTTGCG TGA CTGGCT TGGAGACTCC GAATCCCGGA ATCAACTTGC
** ***** ***** ***** *** * ** * *****
301 : TCTGCCTGTC TCAATTTGCG TGA CTGGCT TGGCGGCTAC GAATCCCGGA ATCAACTTGT

361 : GCTAAGGACA TCCAAAAGGC GCGGCTGAA GCTGCGTTGG CGTTTCAGGA TGAGATGTGT
** ***** * ***** ***** ** *****
361 : GCCAAGGAAA TCCAAAAGGC GCGGCTGAA GCCGCGTTGA ATTTTCAAGA TGAGATGTGT

421 : GATGCGACGA CGGA---TCA TGGCTTCGAC ATGGAGGAGA CGTTGGTGA GGCTATTTAC
** ***** * ** * ** * ***** * *****
421 : CATATGACGA CGGATGCTCA TGGCTTCGAC ATGGAGGAGA CTTGGTGA GGCTATTTAT

478 : ACGGCGGAAC AGAGCGAAAA TGCCTTTTAT ATGCACGATG AGGCGATGTT TGAGATGCCG
*** ***** * * ***** *** * ** * *****
481 : ACGGCGGAAC AGAGCCAAGA TGCCTTTTAT ATGGATGAAG AGGCGATGTT GGGGATGTCT

538 : AGTTTGTGG CTAATATGGC AGAAGGGATG CTTTGGCCG TTCCGTCCGT ACAGTGGAAT
***** ** ***** ***** ***** **
541 : AGTTTGTGG ATAACATGGC CGAAGGGATG CTTTACCGT CGCCGTCGGT TCAATGGAAC

Fig. 2-3

0009114

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598 : CATAATCATG AAGTCGACGG CGATGATGAC GACGTATCGT TATGGAGTTA TTAA
      ***** ** * ***** ** ***** ***** ** * ***** ** ****
601 : TATAATTTTG ATGTCGAGGG AGATGAT--- GACGTGTCCT TATGGAGCTA TTAA

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```

Sequence 1      : DREB1A.nuc
Size            : 651
Matching Position : 1 - 651

```

```

Sequence 2      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 68.72 [%]
Weight            : -233

```

```

1 : ATGAACTCAT TT---TCTGC TTTTCTGAA ATGTTT---- --GGCTCCGA TTACGAGTCT
   ***** ** * ***** ** ***** ***** ** * ***** ** ****
1 : ATGAATCCAT TTTACTCTAC ATTCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT

52 : TCGGTTTCCT CAGGCGGTGA TTATATTCCG ACGCTTGCGA GCAGCTGCCC CAAGAAACCG
   ***** * ***** * * ** * * * * ** * * * * *****
61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTAGCTT CAAGTTGTCC AAAGAAACGA

112 : GCGGGTCGTA AGAAGTTTCG TGAGACTCGT CACCCAATAT ACAGAGGAGT TCGTCGGAGA
   ** ** * * ***** ***** ** ** ** * ***** ***** **
121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG

172 : AACTCCGGTA AGTGGGTTTG TGAGGTTAGA GAACCAAACA AGAAAACAAG GATTTGGCTC
   ** ** ***** * ***** ** ** ** * ***** * ** ***** *
181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTTGGTTA

232 : GGAACATTTT AAACCGCTGA GATGGCAGCT CGAGCTCAGC ACGTTGCCGC TTTAGCCCTT
   ** ** ***** ** * *** ***** ** ** ***** * * ***** ** ***** **
241 : GGTACTTTTC CGACGGTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT

292 : CGTGGCCGAT CAGCCTGTCT CAATTCGCT GACTCGGCTT GGAGACTCCG AATCCCGGAA
   ***** ** * * ***** ***** ***** ** ** ***** ** * ** ** ** ** ** **
301 : CGTGGTCGCT CTGCTTGTCT CAATTCGCT GATTCTGCTT GCGGCTTCG TATTCCTGAG

352 : TCAACTTGGC CTAAGGACAT CAAAAGGCG GCGGCTGAAG CTGCGTTGGC GTTTCAGGAT
   * ***** ***** ** ** ** ** ***** ***** ***** ***** *****
361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT

412 : GAGA----- -TGTGTGAT- ----GCGACG ACGGA-TCA- TGGCTTCGAC A-TGGAGGAG
   **** * * *** * ** ***** ** ** ***** ** * * * * *****
421 : GAGACTACGA CGGAGGGATC TAAAACTGCG GCGGAGGCAG AGGAGGCGGC AGGGGAGGGG

457 : ACGTTGGTGG AGGCTATTTA CACGGCGGAA CAGAGCGAAA ATGCGTTTTA TATGCACGAT
   * ** ** ** * ** ***** ***** * ** ***** ***** * ***
481 : GTGAGGGAGG GGGAGAGGAG GGCGGAGGAG CAGAATGGTG GTGTGTTTA TATGGATGAT

517 : GAGGCGATGT TTGAGATGCC GAGTTTGTG GCTAATATGG CAGAAGGGAT GCTTTTGCCG
   ***** * * * * ***** * ** ** * ***** * ** ***** *****
541 : GAGGCCCTTT TGGGGATGCC CAACTTTTTT GAGAATATGG CGGAGGGGAT GCTTTTGCCG

```

Fig. 2-4

0009114

```

577 : CTTCCGTCCG TACAGTGGAA TCATAATCAT GAAGTCGACG GCGATGATGA CGACGTATCG
      * *** * * ***** * ** * **** * * * * **** *
601 : CCGCCGGAAG TTGGCTGGAA TCATA---AC GACTTTGACG GAG-TG--GG TGACGTGTCA

637 : TTATGGAGTT -----ATTA A
      * ***** * ** *
655 : CTCTGGAGTT TTGACGAGTA A

```

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```

Sequence 1      : DREB1A.nuc
Size            : 651
Matching Position : 1 - 651

```

```

Sequence 2      : DREB1E.nuc
Size            : 546
Matching Position : 1 - 546

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 54.70 [%]
Weight       : 0

```

```

1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTC-
   ***                ****                ***      * * *
1 : ATG----- -----GAAA-----ACGA---CGATATCA

60 : CTCAGGCGGT GATTATATTC CGACGCTTGC GAGCAGCTGC CCCAAGAAAC CGGCGGGTCG
   * ***** * * * * * * * * * * * * * * * *
20 : CCGTGGCGGA GAT-----GAA-----CCTAAGAAC GTGCTGGACG

120 : TAAGAAGTTT CGTGAGACTC GTCACCCAAT ATACAGAGGA GTTCGTCGGA GAAACTCCGG
     * * * * * * * * * * * * * * * * * * * * *
57 : GAGGATTTTC AAGGAGACAC GTCACCCAAT CTACAGAGGC GTGCGGCGTA GGGACGGCGA

180 : TAAGTGGGTT TGTGAGGTTA GAGAACCAAA CAAGAAAACA AGGATTTGGC TCGGAACATT
     ** ***** ** * * * * * * * * * * * * * *
117 : CAAATGGGTA TGCGAAGTCC GTGAACCGAT TCATCAGCGT CGAGTCTGGC TCGGAACCTA

240 : TCAAACCGCT GAGATGGCAG CTCGAGCTCA CGACGTTGCC GCTTAGCCCC TTCGTGGCCG
     ** * * * * * * * * * * * * * * * * * * *
177 : TCCGACGGCA GATATGGCCG CACGTGCTCA CGACGTGGCG GTTCTTGCTC TGCGCGGGAG

300 : ATCAGCCTGT CTCAATTTCT CTGACTCGGC TTGGAGACTC CGAATCCCGG AATCAACTTG
     *** * * * * * * * * * * * * * * * * * * *
237 : ATCCGCGTGT TTGAATTTCT CCGATTCTGC TTGGAGGTTG CCGGTGCCCG CATCCACT--

360 : CGCTAAGGAC ATCCAAAGG ----CGGCGG CTGAAGCTGC GTTGGCGTTT CAGGATG-AG
     * * **** * * * * * * * * * * * * * * *
295 : -GATCCGGAC A-CGATCAGG CGCAGGCGCG CCGAAGCAGC GGAGATG-TT CAGGCCGCGG

415 : ATGTGTGATG CGACGACGGA TCATGGCTTC GACATGGAGG AGACGTTGGT GGAGGCTATT
     * * * * * * * * * * * * * * * * * * *
352 : GAGT-TTAGT --AC-AGGAA TTACGGTTTT ACCCT----C AGCC---AGT -GAG---TTT

475 : TACACGGCGG AACAGAGCGA AAATGCGTTT TATATGCACG ATGAGGCGAT GTTTGAGATG

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Fig. 2-5

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***** *** * ** * * *** * * *** * * ***** * *** *
397 : GACACGTCGG A--TGA---A GGAGTCGCTG GA-ATG-ATG ATGAGGC--T CGCGGAGGAG

535 : CCGAGTTTGT TG--GCTAAT ATGGCAGA-A GGGATGCTTT TGCCGCTTCC GTCCGTACAG
*** *** * ** ** * * * * * * * * * * * * * * * *
448 : CCGTTGATGT CGCCGCCAAG ATCGTACATT GATATG-AAT --ACG----A GTGTGTAC-G

592 : TGGAAATCATA ATCATGAAGT CGACGGCGAT GATGACGACG TATCGTTATG GAGTTATTAA
**** * * * *** * * * * * * * * * * * * * * * *
500 : TGGACGAAGA A--ATG-----TGT TACGAAGATT TGTCACTTTG GAGTTACTAA

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Sequence 1          : DREB1A.nuc
Size                : 651
Matching Position   : 1 - 651

Sequence 2          : DREB1F.nuc
Size                : 630
Matching Position   : 1 - 630

Matching Condition.

Matches             : -1
Mismatch           : 1
Gaps                : 1
*N+                 : 2

Matching            : 54.81 [%]
Weight              : -21

1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTCC
**** * * * * * * * * * * * * * * * *
1 : ATGAA-----TAATG AT-----G AT-----ATTAT

61 : TCAGGCGGTG ATTATATTCC GACGCTTGGC AGCAGCTGCC CCAAGAAACC GGCGGGTCGT
** ***** * * * * * * * * * * * * * * * *
21 : TCTGCGGAG AT-----G A-----GGC CTAAGAAGCG TCGGGAAGG

121 : AAGAAGTTTC GTGAGACTCG TCACCAATA TACAGAGGAG TTCGTCGGAG AAATCCGGT
* **** * * * * * * * * * * * * * * * * * * *
58 : AGAGTGTITA AGGAGACACG TCACCCAGTT TACAGAGGCA TAAGGCGGAG GAACGGTGAC

181 : AAGTGGGTTT GTGAGGTTAG AGAACCAAAC AAGAAAACAA GGATTGGCT CGGAACATT
** ***** * * * * * * * * * * * * * * * *
118 : AAATGGGTCT GCGAAGTCAG AGAACCGACG CACCAACGCC GCATTGGCT CGGGACTTAT

241 : CAAACCGCTG AGATGGCAGC TCGAGCTCAC GACGTTGCCG CTTTAGCCCT TCGTGGCCGA
* ** * * * * * * * * * * * * * * * * * * *
178 : CCCACAGCAG ATATGGCAGC GCGTGCACAC GACGTGGCGG TTTAGCTCT GCGTGGGAGA

301 : TCAGCCTGTC TCAATTTGCG TGACTCGGCT TGGAGACTCC GAATCCCGGA ATCAACTTGC
** ** * * * * * * * * * * * * * * * * * *
238 : TCCGCATGTT TGAATTTGCG CGACTCCGCT TGGCGGCTTC CGTGCCCGGA ATCCAATGAT

361 : GCTAAGGACA TCCAAAAGGC GGCGGCTGAA GCTGCGTTGG CGTTTCAGGA TG--AGATGT
* * * * * * * * * * * * * * * * * * * *
298 : CCGGATGTGA TAAGAAGAGT TCGGCGGAA GCTGCGGAGA TGTTT-AGGC CGGTGATT

419 : -GTGA-TGCG ACGACGGATC ATGGCTT--- --CGACATGG AGGAGACGTT GGTGGAGGCT
* * * * * * * * * * * * * * * * * * *
357 : AGAAAGTGA ATTACGG-TT TTGCCTTGTG CGGGAGATGA TGTGGATTG GGTTTTGGTT

```

Fig. 2-6

0009114

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472 : ATTTACACGG C----- GGAACAGA-G CGA-AAATGC GT-TTTATAT GCACGATGAG
      *** *          *** * * * * * * * * * * * * * * * *
416 : CGGGTTCCGG CTCTGGTTCC GGATCGGAGG AGAGGAATC TTCTTCGTAT GGATTGGAG

520 : GCGATGTTTG AGATGCCGAG TTTGTTGGCT AATATGGCAG AAGGGATGCT TTTGCCGCTT
      * * * * * * * * * * * * * * * * * * * * * *
476 : ACTACG-AAG AAGTCTCAAC GACGATGATG AGACTCGCGG AGGGGCCACT AATGTCGCCG

580 : C--CGTCCGT ACAGTGGA-- -----TCA TAATCATG-- -AAGTCGACG --GCGATG--
      * ** *** * * * * * * * * * * * * * * * * * *
535 : CCGCGATCGT ATA-TGGAAG ACATGACTCC TACTAATGTT TACACGGAAG AAGAGATGTG

623 : --ATGACGAC GTATCGTTAT GGAGT----- -TATTAA
      **** ** * * * * * * * * * * * * * * *
594 : TTATGAAGAT ATGTCATTGT GGAGTTACAG ATATTAA

```

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```

Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642

```

```

Sequence 2      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*Nt          : 2

Matching      : 86.33 [%]
Weight       : -471

```

```

1 : ATGAAGTCAT TTTCAGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGCC TC-----
    ***** * * * * * * * * * * * * * * * * * *
1 : ATGAAGTCAT TTCTGCCTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TCCGGTTTCC

53 : -AAGCGGAG ATTATTGTCC GACGTTGGCC ACGAGTTGTC CGAAGAAACC GCGGGGCCGT
    ***** * * * * * * * * * * * * * * * * *
61 : TCAGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAG

112 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAATCCGGT
    ***** * * * * * * * * * * * * * * * * *
121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAATCCGGT

172 : AAGTGGGTTT CTGAAGTGAG AGAGCCAAAC AAGAAAACCA GGATTGGCT CGGGACTTTC
    ***** * * * * * * * * * * * * * * * * *
181 : AAGTGGGTGT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGATTGGCT CGGGACTTTC

232 : CAAACCGCTG AGATGGCAGC TCGTGCTCAC GACGTCGCTG CATTAGCCCT CCGTGGCCGA
    ***** * * * * * * * * * * * * * * * * *
241 : CAAACCGCTG AGATGGCAGC TCGTGCTCAC GACGTCGCCG CCATAGCTCT CCGTGGCAGA

292 : TCAGCATGTC TCAACTTCGC TGAATCGGCT TGGCGGCTAC GAATCCCGGA GTCAACATGC
    ** * * * * * * * * * * * * * * * * *
301 : TCTGCCTGTC TCAATTCGC TGAATCGGCT TGGCGGCTAC GAATCCCGGA ATCAACCTGT

352 : GCCAAGGATA TCCAAAAGC GGCTGCTGAA GCGGCGTTGG CTTTCAAGA TGAGACGTGT
    ***** * * * * * * * * * * * * * * *

```


Fig. 2-7

0009114

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361 : GCCAAGGAAA TCCAAAAGGC GCGGCTGAA GCCGCGTTGA ATTTTCAAGA TGAGATGTGT

412 : GATACGACGA CCACGAATCA TGGCCTGGAC ATGGAGGAGA CGATGGTGA AGCTATTTAT
    *** ***** *      *** ** ** * ***** * ***** *****
421 : CATATGACGA CGGATGCTCA TGGTCTTGAC ATGGAGGAGA CCTTGGTGA GGCTATTTAT

472 : ACACCGGAAC AGAGCGAAGG TGCCTTTTAT ATGGATGAGG AGACAATGTT TGGGATGCCG
    ** ***** ***** *** ***** * ** * ***** ***** *
481 : ACGCCGGAAC AGAGCCAAGA TGCCTTTTAT ATGGATGAAG AGGCGATGTT GGGGATGTCT

532 : ACTTTGTTGG ATAATATGCG TGAAGGCATG CTTTACCGC CGCCGTCTGT TCAATGGAAT
    * ***** ***** ***** *** ***** ***** ** *****
541 : AGTTTGTGG ATAACATGCG CGAAGGGATG CTTTACCGT CGCCGTCTGT TCAATGGAAC

592 : CATAATTATG ACGGCGAAGG AGATGGTGAC GTGTCGCTTT GGAGTTACTA A
    ***** ** * * *** ** ***** ***** ***** * * **** ** ** *
601 : TATAATTTTG ATGTCGAGGG AGATGATGAC GTGTCCTTAT GGAGCTATTA A
  
```

+++++

```

Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642
  
```

```

Sequence 2      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 68.88 [%]
Weight       : -234
  
```

```

1 : ATGAACTCAT TT---TCAGC TTTTCTGAA ATGTTT---- --GGCTCCGA TTA-CGAGC-
    ***** ** ** ** * ** * ** **** ***** * * ** *
1 : ATGAATCCAT TTACTCTAC ATTCCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT

50 : -----CTC AAGGCGGAGA TTATTGTCCG ACGTTGGCCA CGAGTTGTCC GAAGAAACCG
    * * * * * * ** * * * ** * ** * * *****
61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA

103 : GCGGGCCGTA AGAAGTTTCG TGAGACTCGT CACCCAATTT ACAGAGGAGT TCGTCAAAGA
    ** ** * * ***** ***** ** ** **** ***** ***** **
121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG

163 : AACTCCGGTA AGTGGGTTTC TGAAGTGAGA GAGCCAACA AGAAAACCAG GATTGGCTC
    ** ** **** * ***** ***** *** ***** ** * ***** * ** *****
181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTGGTTA

223 : GGGACTTTCC AAACCGCTGA GATGGCAGCT CGTGCTCAGC ACGTCGCTGC ATTAGCCCTC
    ** ***** * ** * *** ***** ***** * * ** ***** *****
241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT

283 : CGTGGCCGAT CAGCATGTCT CAACTTCGCT GACTCGGCTT GCGGGCTACG AATCCCGGAG
    ***** ** * * ** ***** ** ***** ** ** ***** ** ** ** **
301 : CGTGGTCGCT CTGCTTGCTCT CAATTCGCT GATTCTGCTT GCGGGCTTCG TATTCCTGAG
  
```

Fig. 2-8

0009114

```

343 : TCAACATGCG CCAAGGATAT CCAAAAAGCG GCTGCTGAAG CGGCGTTGGC TTTTCAAGAT
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGCC GTTTCAGAAAT

403 : GAGAC----- --GTGTGA-- TACGACGACC AC-GAATCA- TGGCCTGGAC A-TGGAGGAG
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
421 : GAGACTACGA CGGAGGGATC TAAAACTGCG GCGGAGGCAG AGGAGGCGGC AGGGGAGGGG

451 : ACGATGGTGG AAGCTATTTA TACACCGGAA CAGAGCGAAG GTGCGTTTTA TATGGATGAG
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
481 : GTGAGGGAGG GGGAGAGGAG GCGGAGGAG CAGAATGGTG GTGTGTTTTA TATGGATGAT

511 : GAGACAATGT TTGGGATGCC GACTTTGTTG GATAATATGG CTGAAGGCAT GCTTTTACCG
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
541 : GAGGCGCTTT TGGGGATGCC CAACTTTTTT GAGAATATGG CGGAGGGGAT GCTTTTGCCG

571 : CCGCCGCTCG TTCAATGGAA TCATAATTAT GACGGCGAAG GAGATGGTGA CGTGTGCGTT
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
601 : CCGCCGGAAG TTGGCTGGAA TCATA---AC GACTTTGACG GAGTGGGTGA CGTGTCACTC

631 : TGGAGTT--- ---ACTAA
      * * * * * * * * * *
658 : TGGAGTTTTG ACGAGTAA
  
```

+++++

```

Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642

Sequence 2      : DREB1E.nuc
Size            : 546
Matching Position : 1 - 546
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 53.38 [%]
Weight            : 2
  
```

```

1 : ATGAACTCAT TTTCAGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGCC TCAAGGCGGA
   ***          ****          * ** * * * * * * * * *
1 : ATG----- -----GAAA-- ----ACGACG AT----ATCA CCGTGGCGGA

61 : GATTATTGTC CGACGTTGGC CACGAGTTGT CCGAAGAAAC CGGCGGGCGG TAAGAAGTTT
   ***          **          **          ** * * * * * * * * *
30 : GAT----- -GA----- ----AG----- CCAAGAAGC GTGCTGGACG GAGGATTTTC

121 : CGTGAGACTC GTCACCCAAT TTACAGAGGA GTTCGTCAAA GAAACTCCGG TAAGTGGGTT
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
67 : AAGGAGACAC GTCACCCAAT CTACAGAGGC GTGCGGCGTA GGGACGGCGA CAAATGGGTA

181 : TCTGAAGTGA GAGAGCCAAA CAAGAAAACC AGGATTTGGC TCGGGACTTT CCAAACCGCT
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
127 : TCGGAAGTCC GTGAACCGAT TCATCAGCGT CGAGTCTGGC TCGGAACTTA TCCGACGGCA

241 : GAGATGGCAG CTCGTGCTCA CGACGTCGCT GCATTAGCCC TCCGTGGCGG ATCAGCATGT
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
187 : GATATGGCCG CACGTGCTCA CGACGTGGCG GTTCTTGCTC TCGCGGGGAG ATCCGCGTGT
  
```

Fig. 2-9

0009114

```

301 : CTCAACTTCG CTGACTCGGC TTGGCGGCTA CGAATCCCGG AGTCAAC--A TGCGCCAAGG
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
247 : TTGAATTTCT CCGATTCTGC TTGAGGTTG CCGGTGCCGG CATCCACTGA TCCGGACACG

359 : AT-ATCCAAA AAGCGGCTGC TGAAGCGGCG TTGGCTTTTC AAGATG-AGA CGTGTGATAC
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
307 : ATCAGGCGCA ---CGGCGGC CGAAGCAGCG -GAGATGTT AGGCCGCCGG AGTTTAGTAC

417 : GACGACCACG AATCATGGCC T-GGACATGG AG---GAGAC GATGGTGGA GCTATTTATA
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
363 : AGGAATTACG -GTTTTACCC TCAGCCAGTG AGTTTGACAC GTCGGATGAA G-----GAGT

473 : CACCGGAACA GAGCGAAGGT GCGTTTTATA TGGATGAGGA GACAATGTTT GGGATGCCGA
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
417 : CGCTGGAA-- ---TGATGAT GAG-----GC TCGCGGAGGA GCCGTGTATG TCGCCGCCAA

533 : CTTTGTGGA TAATATGGCT GAAGGCATGC TTTTACCGCC GCCGTCTGTT CAATGGAATC
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
467 : GATCGTACAT TGATA----T GAA----- ---TAC---- -GAGTGTGA C-GTGGACGA

593 : ATAATTATGA CGGCGAAGGA GATGGTGACG TGTCGCTTTG GAGTTACTAA
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
507 : AGAAATGTG- TTACGAA--- -----GATT TGTCACITTG GAGTTACTAA

```

+++++

```

Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642

Sequence 2      : DREB1F.nuc
Size            : 630
Matching Position : 1 - 630

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*NT         : 2

Matching      : 56.23 [%]
Weight       : -34

```

```

1 : ATGAACTCAT TTTACGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGCC TCAAGGCGGA
      ***** * * * * * * * * * * * * * * * * * * * * * * * *
1 : ATGAA-TAAT GATGATATTA TTCT----- -----GCGCGGA

61 : GATTATTGTC CGACGTTGGC CACGAGTTGT CCGAAGAAAC CGGCGGGCCG TAAGAAGTTT
      *** * * * * * * * * * * * * * * * * * * * * * * *
30 : GAT----- ---GA---GG CCTAAGAAGC GTGCGGGAAG GAGAGTGTTC

121 : CGTGAGACTC GTCACCCAAT TTACAGAGGA GTTCGTCAAA GAAACTCCGG TAAGTGGGTT
      ***** * * * * * * * * * * * * * * * * * * * * * *
67 : AAGGAGACAC GTCACCCAGT TTACAGAGGC ATAAGGCGGA GGAACGGTGA CAAATGGGTC

181 : TCTGAAGTGA GAGAGCCAAA CAAGAAAACC AGGATTGGC TCGGGACTTT CCAAACCGCT
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *
127 : TCGGAAGTCA GAGAACCACG GCACCAACGC CGCATTGGC TCGGGACTTA TCCACAGCA

241 : GAGATGGCAG CTCGTGCTCA CGACGTCGCT GCATTAGCCC TCCGTGGCCG ATCAGCATGT

```

Fig. 2-10

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```

** ***** * ***** ** ***** ** * ***** * * ***** * *** *****
187 : GATATGGCAG CGCGTGCACA CGACGTGGCG GTTTTAGCTC TCGGTGGGAG ATCCGCATGT

301 : CTCAACTTCG CTGACTCGGC TTGGCGGCTA CGAATCCCGG AGTCAACATG CGCC-AAGGA
      * * ***** * ***** ** ***** * * ***** * * * * * * * *
247 : TTGAATTTTCG CCGACTCCGC TTGGCGGCTT CCGGTGCCGG AATCCA-ATG ATCCGGATGT

360 : TATCCAAAAA GCGGCTGCTG AAGCGGCGTT GGCTTTTCAA GATGAGACGT GTGATACGAC
      ** ** * * * * * * * * * * * * * * * * * * * * * * * *
306 : GATAAGAAGA GTTGCGGCGG AAGCTGCGGA GATGTTTAGG CCGGTGGATT TAGAAAGTGG

420 : GACCACGAAT ----CATGGC CTGGACATG- -GAGGA---- GACGATGGT- --GG---AAG
      * * * * * * * * * * * * * * * * * * * * * * * *
366 : AATTACGGTT TTGCCTTGTG CGGGAGATGA TGTGGATTG GGTTTTGGTT CGGGTTCCGG

464 : CTAT--TTAT ACACCGGAAC AGAGCGAAGG TGCCT-TTTA TATGGATGAG GAGACAATGT
      ** * * * * * * * * * * * * * * * * * * * * * * * *
426 : CTCTGGTTCG GGATCGGAGG AGAG-GAA-- TTCTTCTTCG TATGGATTG GAGACTACG-

521 : TTGGGATGCC GACTTTGTTG GATAATA-TG GCTGAAGG-- CA-TGCTTTT ACCGCCCGC--
      * * * * * * * * * * * * * * * * * * * * * * * *
482 : AAGAAGTCTC AACGACGAT- GATGAGACTC GCGGAGGGGC CACTAATGTC GCCGCCGCGA

575 : -CGTCTGTTT AA---TGGAA TCATAATTAT G-----ACGG CGAAGGAGAT G-GT-----
      *** * * * * * * * * * * * * * * * * * * * * * * *
541 : TCGTATATGG AAGACATGAC TCCTACTAAT GTTTACACGG AAGAAGAGAT GTGTTATGAA

619 : GACGTGTCGC TTTGGAGTTA C-----TAA
      ** ***** * ***** * * *
601 : GATATGTCAT TGTGGAGTTA CAGATATTAA

```

+++++

```

Sequence 1      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651

```

```

Sequence 2      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 68.34 [%]
Weight            : -233

```

```

1 : ATGAACTCAT TT---TCTGC CTTTCTGAA ATGTTT---- --GGCTCCGA TTACGAGTCT
      ***** ** * * * * * * * * * * * * * * * * * *
1 : ATGAATCCAT TTTACTCTAC ATTCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT

52 : CCGGTTTCTT CAGGCGGTGA TTACAGTCCG AAGCTTGCCA CGAGCTGCCC CAAGAAACCA
      ***** * * * * * * * * * * * * * * * * * *
61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA

112 : GCGGGAAGGA AGAAGTTTCG TGAGACTCGT CACCCAATTT ACAGAGGAGT TCGTCAAAGA
      ** ** ***** ***** * * * * * * * * * * * *
121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATT ACAGAGGAGT TCGTCAGAGG

```

Fig. 2-11

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```

172 : AACTCCGGTA AGTGGGTGTG TGAGTTGAGA GAGCCAAACA AGAAAACGAG GATTTGGCTC
    ** ** ** * ** ** ** * ** * ** * ** * ** * ** * **
181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTTGGTTA

232 : GGGACTTTCC AAACCGCTGA GATGGCAGCT CGTGCTCACG ACGTCGCCGC CATAGCTCTC
    ** ** ** * ** * ** * ** ** ** * ** * ** * ** * **
241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT

292 : CGTGGCAGAT CTGCCTGTCT CAATTTGCTT GACTCGGCTT GGCGGCTACG AATCCCGGAA
    ***** * * ** * ** * ** * ** * ** * ** * ** * **
301 : CGTGGTCGCT CTGCTTGTCT CAATTTGCTT GATTCTGCTT GGCGGCTTCG TATTCCTGAG

352 : TCAACCTGTG CCAAGGAAAT CCAAAGGCG GCGGCTGAAG CCGCGTTGAA TTTTCAAGAT
    * ** ** * ** ** * ** ** ** * ** * ** * ** * ** * **
361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT

412 : GAGA----- -TGTGTCATA TGA-----CG ACGGATGCTC ATGGTCTTGA CA-TGGAGGA
    **** : * * ** * * ** * ** * ** * ** * ** * **
421 : GAGACTACGA CGGAGGGATC TAAACTGCG GCGGAGGCAG A-GGAGGCGG CAGGGGAGGG

459 : GACCTTGGTG GAGGCTATTT ATACGCCGGA ACAGAGCCAA GATGCGTTTT ATATGGATGA
    * ** * ** * ** * ** * ** * ** * ** * ** * ** * **
480 : GGTGAGGGAG GGGGAGAGGA GGGCGGAGGA GCAGAATGGT GGTGTGTTTT ATATGGATGA

519 : AGAGGCGATG TTGGGGATGT CTAGTTTGTG GGATAACATG GCCGAAGGGA TGCTTTTACC
    ***** * ***** * * ** ** * ** * ** * ** * **
540 : TGAGGCGCTT TTGGGGATGC CCAACTTTTT TGAGAATATG GCGGAGGGGA TGCTTTTACC

579 : GTCGCCGTCG GTTCAATGGA ACTATAATTT TGATGTCGAG GGAGATGATG ACGTGTCTCT
    * **** * ** * ** * ** * ** * ** * ** * ** * ** *
600 : GCCGCCGGA GTTGGCTGGA ATCATAA--- CGACTTTGAC GGAGTGGTG ACGTGTCACT

639 : ATGGAG---- --CTATTAA
    ***** * * **
657 : CTGGAGTTTT GACGAGTAA

```

+++++

```

Sequence 1      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651

```

```

Sequence 2      : DREB1E.nuc
Size            : 546
Matching Position : 1 - 546

```

Matching Condition.

```

Matches          : -1
Mismatched       : 1
Gaps             : 1
*N+              : 2

Matching         : 54.95 [%]
Weight          : 1

```

```

1 : ATGAACTCAT TTTCTGCCTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TCCGGTTTCC
    ***                ****          * ** **          ** ***
1 : ATG----- -----GAAA-- ----ACGACG AT-----ATC ACCG-----

61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAGG
    ***** * **          ****                * * ***** * ** *** **

```

Fig. 2-12

```

                                0009114
23 : --TGGCGGAG AT----- GAAG----- -----C CAAAGAAGCG TGCTGGACGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAAC TCCGGT
      * ** **      ***** ** ***** ***** * * ** * ** ** **
58 : AGGATTTTCA AGGAGACACG TCACCCAATC TACAGAGGCG TCGGCGTAG GGACGGCGAC

181 : AAGTGGGTGT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGA-TTTGGC TCGGGACTTT
      ** ***** * * ** * * ** ** * * ** ** * **** **** ****
118 : AAATGGGTAT GCGAAGTCCG TGAACCGATT CA-TCAGCGT CGAGTCTGGC TCGGAACTTA

240 : CCAAACCGCT GAGATGGCAG CTCGTGCTCA CGACGTGCGC GCCATAGCTC TCCGTGGCAG
      * ** ** ** ***** * ***** ***** ** * * **** * ** **
177 : TCCGACGGCA GATATGGCCG CACGTGCTCA CGACGTGGCG GTTCTTGCTC TCGCGGGAG

300 : ATCTGCCTGT CTCAATTTCT CTGACTCGGC TTGGCGGCTA CGAATCCCGG AATCAACCTG
      *** ** *** * ***** * ** ** ** **** ** * * * **** **** *
237 : ATCCGCGTGT TTGAATTTCT CCGATTCTGC TTGGAGGTTG CCGGTGCCGG CATCCA-CTG

360 : TGCCAAGGAA ATCCAAAAGG ----CGGCGG CTGAAGCCGC GTTGAATTTT CAAGATGAGA
      ** *** * * * *** ***** * ***** * * * **** ** *
296 : ATCC--GGAC A-CGATCAGG CGCACGGCGG CCGAAGCAGC GGAG-ATGTT CAGGCCG-CC

416 : TGTGTCATAT GACGACGGAT GCTCATGGTC TTGACATGGA GGAGACCTTG GTGGAGGCTA
      * ** ** ** *** * * **** ** * * ** ** ** ** **
351 : GGAGT-TTAG TAC--AGGA- -ATTACGGT TTACCCT--- -CAG-CC--A GT-GAG---T

476 : TTTATACGCC GGAACAGAGC CAAGATGCGT TTTATATGGA TGAAGAGGCG ATGTTGGGGA
      ** * *** * *** ** * ** ** * * ** ** ** ***** * * ***
395 : TTGACACGTC GGA--TGA-- -AGGAGTCGC TGA-AT-GA TGATGAGGC- ---TCGCGGA

536 : TGTCTAGTTT GT-TGGATAA CATGGCCGAA GGGATGCTTT TACCGTCGCC GTCGGTTCAA
      * *** * * * ** * * ** * * ** * * * ** **
444 : GGAGCCGTTG ATGTCGCCGC CAAGATCGTA -CATTGATAT GA--ATACGA GTGTGTAC-G

595 : TGGAACTATA ATTTTGATGT CGAGGGAGAT GATGACGTGT CCTTATGGAG CTATTAA
      **** * * * **** * * ** ** ** * * **** * * ***
500 : TGGACGAAGA A-----ATGT -----GTTAC GAAGATTTGT CACTTGGAG TTACTAA

```

+++++

```

Sequence 1      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651

```

```

Sequence 2      : DREB1F.nuc
Size            : 630
Matching Position : 1 - 630

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps              : 1
* N t            : 2

Matching         : 56.10 [%]
Weight           : -35

```

```

1 : ATGAACTCAT TTTCTGCCCTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TCCGGTTTCC
   ****              **** *      * **              **
1 : ATGAA----- -----TAATG AT-----G AT-----ATTAT

```

Fig. 2-13

-0009114

```

61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAGG
    ** ***** * **                ** * * * ***** * *****
21 : TCTGGCGGAG AT----- --GA---GGC CTAAGAAGCG TCGGGAAGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAACCTCCGGT
    * **** * * * * * * * * * * * * * * * * * * * * * * * *
58 : AGAGTGTTTA AGGAGACACG TCACCCAGTT TACAGAGGCA TAAGGCGGAG GAACGGTGAC

181 : AAGTGGGTGT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGATTGGCT CGGGACTTTC
    ** ***** * * * * * * * * * * * * * * * * * * * * * *
118 : AAATGGGTCT GCGAAGTCAG AGAACCAGCG CACCAACGCC GCATTGGCT CGGGACTTAT

241 : CAAACCGCTG AGATGGCAGC TCGTGCTCAC GACGTCGCCG CCATAGCTCT CCGTGGCAGA
    * * * * * * * * * * * * * * * * * * * * * * * * * * *
178 : CCCACAGCAG ATATGGCAGC GCGTGCACAC GACGTGGCGG TTTTAGCTCT GCGTGGGAGA

301 : TCTGCCTGTC TCAATTTTCG TGAATTCGCT TGGCGGCTAC GAATCCCGGA ATCAACCTGT
    ** ** * * * * * * * * * * * * * * * * * * * * * * *
238 : TCCGCATGTT TGAATTTTCG CCACTCCGCT TGGCGGCTTC CGGTGCCGGA ATCCAATGAT

361 : GCCAAGGAAA TCCAAAAGGC GCGGGCTGAA GCCGCGTTGA ATTTTCAAGA TG--AGATGT
    * * * * * * * * * * * * * * * * * * * * * * * * *
298 : CCGGATGTGA TAAGAAGAGT TCGGGCGGAA GCTGCGGAG- ATGTTTAGGC CGGTGGATT

419 : GTCATATG-- ACGACGGATG CTCATGGT-C TTGACATG-- GAGGA----G ACCTTGGTGG
    * ** * * * * * * * * * * * * * * * * * * * * *
357 : AGAAAGTGGA ATTACGGTTT TGCCTTGTGC GGGAGATGAT GTGGATTGG GTTTTGGTTC

470 : AGGCTATTTA TACG---CCG GAACAGAGCC AAG--ATGCG T-TTTATATG GATGAAGAGG
    ** * * * * * * * * * * * * * * * * * * * * * *
417 : GGGTTCGGC TCTGGTTCGG GATCGGAGGA GAGGAATTCT TCTTCGTATG GATTGGGAGA

524 : CGATGTTGGG GATGTCTAGT TTGTTGGATA ACA-TGGCCG AAGGGATGCT TTTACCGTCC
    * * * * * * * * * * * * * * * * * * * * * * *
477 : CTACGAAGAA G-TCTCAACG ACGAT-GATG AGACTCGCGG AGGGGCCACT AATGTCGCCG

583 : CCGTCGGT-- TCAATGGAA- -----C TA-TAATTTT GATGTCGAGG --GAGATG--
    *** ** * * * * * * * * * * * * * * * * * * *
535 : CCG-CGATCG TATATGGAAG ACATGACTCC TACTAATGTT TACACGGAAG AAGAGATGTG

626 : --ATGACG-- -TGTCTTAT GG-----AG CTATTAA
    **** * **** * * * * * * * *
594 : TTATGAAGAT ATGTCATTGT GGAGTTACAG ATATTAA
  
```

+++++

```

Sequence 1      : DREB1D.nuc
Size           : 675
Matching Position : 1 - 675
  
```

```

Sequence 2      : DREB1E.nuc
Size           : 546
Matching Position : 1 - 546
  
```

Matching Condition.

```

Matches       : -1
Mismatches    : 1
Gaps          : 1
*N+           : 2

Matching      : 51.26 [%]
Weight       : 29
  
```

Fig. 2-14

0009114

```

1 : ATGAATCCAT TTTACTCTAC ATTCCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT
   ***                **                ** * *** * ***
1 : ATG----- -GA- -AAACGACGA T-----ATCA

61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA
   ** ** * * * **                * *** ** ***** **
20 : CC-GTGGCGG A-----GA -T GAAG----CC AAAGAAGCGT

121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG
   ***** ** ** ** ***** ** ** ** * ***** **
49 : GCTGGACGGA GGATTTTCAA GGAGACACGT CACCCAATCT ACAGAGGCGT GCGGCGTAGG

181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTGGTTA
   * * * ***** ** ***** * ** ** * * * * * *
109 : GACGGCGACA AATGGGTATG CGAAGTCCGT GAACCGATTG ATCAGCGTCG AGTCTGGCTC

241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT
   ** **** ** ***** ** ***** ** * * * * * *
169 : GGAAC TTATC CGACGGCAGA TATGGCCGCA CGTGCTCACG ACGTGGCGGT TCTTGCTCTG

301 : CGTGGTCGCT CTGCTTGCT CAATTCGCT GATTCTGCTT GGCGGCTTCG TATTCCTGAG
   ** ** * * * * * * ***** * ***** ** * * * *
229 : CGCGGGAGAT CCGCGTGTG GAATTTCTCC GATTCTGCTT GGAGGTTGCC GGTGCCGCGA

361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT
   * *** ** * * * * * * * * * * * * * * *
289 : TCCACTGATC CGGACACGAT CAGGCGCAGC GCGGCCGAAG CAGCGGAGAT G-TTCAG---

421 : GAGACTACGA CGGAGGGATC TAAACTGCG GCGGAGGCAG AGGAGGCGGC AGGGAGGGG
   ** ***** * ** ** * * * * * * * * *
345 : -----GCCGC CGGAG---TT TAGTACAG-G AATTA--CGG TTTTACCCTC A-GCCAGTGA

481 : GTGAGGGAGG GGGAGAGGAG GCGGAGGAG CAGAATGGT GTGTGTTTTA TATGGATGAT
   ** * * * * * * * * * * * * * * * * *
393 : GTTTGACACG TCG-GATGAA GGAGTCGCTG --GAATGATG ATGAG----- GCTCGCGGAG

541 : GAGGCGCTTT TGGGATGCC CAACTTTTTT GAGAATATGG CGGAGGGGAT GCTTTTGCCG
   *** ** * ** * * * * * * * * * * * *
445 : GAGCCGTGA TGTGCGCGCC AAGATCGTAC ATTGATAT-- -----GAAT ACGAGTG---

601 : CCGCCGGAAG TTGGCTGGA TCATAACGAC TTTGACGGAG TGGGTGACGT GTCACTCTGG
   * * * * * * * * * * * * * * * * *
494 : ----TGTACG TGGAC--GAA --GAAATG-- TGTTACGAA- -----GATTT GTCAC TTGG

661 : AGTTTTGACG AGTAA
   **** * ***
538 : AGTT----- ACTAA

```

+++++

```

Sequence 1      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675

```

```

Sequence 2      : DREB1F.nuc
Size            : 630
Matching Position : 1 - 630

```

Matching Condition.

Fig. 2-15

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Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2
 Matching : 54.92 [%]
 Weight : -24

```

1 : ATGAATCCAT TTTACTCTAC ATTCCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT
    *****                               *** ** * *** *
1 : ATGAAT----- -AAT-----GA TGATATTATT

61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA
    * * * * * *** * * * * *
22 : CTGG---CGG AGA---TGA -----GGCC TAAGAAGCGT

121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG
    ** ** * * * * * * * * * * * * * * *
49 : GCGGGAAGGA GAGTGTAA GGAGACACGT CACCCAGTTT ACAGAGGCAT AAGCGGAGG

181 : AATTCTGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAATCTAG GATTGTTGTA
    ** * * * * * * * * * * * * * * *
109 : AACGGTGACA AATGGGTCTG CGAAGTCAGA GAACCGACGC ACCAACGCCG CATTGGCTC

241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT
    ** * * * * * * * * * * * * * * *
169 : GGGACTTATC CCACAGCAGA TATGGCAGCG CGTGACACG ACCTGGCGGT TTTAGCTCTG

301 : CGTGGTCGCT CTGCTTGCT CAATTCGCT GATTCTGCTT GGCGGCTTCG TATTCCTGAG
    ***** * * * * * * * * * * * * * * *
229 : CGTGGGAGAT CCGCATGTTT GAATTCGCC GACTCCGCTT GGCGGCTTCC GGTGCCGGA

361 : ACTACTTGTC CTAAGGAGAT TCAGAA-AGC TGCCTCTGAA GCTGCAATGG CGTTTCAGAA
    * * * * * * * * * * * * * * *
289 : TCCAATGATC CGGATGTGA- TAAGAAGAGT TCGCGCGGAA GCTGCGGAGA TGTTTAGGCC

420 : TG-AGACTAC GACGGAGGGA TCTAAACTG CGGC---GGA GGCAGAGGAG GCGG-CAGGG
    * * * * * * * * * * * * * * *
348 : GGTGGATTTA GAAAGTGAA T-TACGGTTT TGCCTTGTC GGGAGATGAT GTGGATTG

475 : GAGGGGGTGA GGG---AGGG GGAGAGGAGG G--CGGAGGA GCAGAATGGT GGTGTGTTT
    * * * * * * * * * * * * * * *
407 : GTTTTGTTTC GGGTTCGGC TCTGGTTCGG GATCGGAGGA GAGGAAT--- --TCTTCTC

530 : ATATGGATGA TGAGGCGCTT TTGGGGATG- CCCAACTTTT TTGA-GAATA TGGCGGAGGG
    ***** * * * * * * * * * * *
462 : GTATGGATTG GGAGAC---T ACGAAGAAGT CTCAACGACG ATGATGAGAC TCGCGGAGGG

588 : GATGCTTTTG CCGCCGCCG- GAAGTTGGCT GGAA-TCATA A---CGAC-- ----TTTGAC
    * * * * * * * * * * * * * * *
519 : GCCACTAATG TCGCCGCCG GATCGTATAT GGAAGACATG ACTCCTACTA ATGTTTACAC

637 : GGA----- --GTG---G GTGACGTGTC ACTCTGGAGT TTTGACGAGT AA
    *** * * * * * * * * * *
579 : GGAAGAAGAG ATGTGTTATG AAGATATGTC ATTGTGGAGT TACAGATATT AA
  
```

+++++

Sequence 1 : DREB1E.nuc
 Size : 546

Fig. 2-16

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Matching Position : 1 - 546
Sequence 2 : DREB1F.nuc
Size : 630
Matching Position : 1 - 630

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2
Matching : 69.26 [%]
Weight : -221

```

1 : ATGGAACACG ACGATATCAC CGTGGCGGAG ATGAAGCCAA AGAAGCGTGC TGGACGGAGG
   *** * ** * * ***** * ***** **** * * ***** *** ****
1 : ATGAATAATG ATGATATTAT TCTGGCGGAG ATGAGGCCTA AGAAGCGTGC GGAAGGAGA

61 : ATTTTCAAGG AGACACGTCA CCAATCTAC AGAGGCGTGC GCGGTAGGGA CGGCGACAAA
   * ** **** ***** **** * ** ***** * **** * * * ** *****
61 : GTGTTTAAGG AGACACGTCA CCCAGTTTAC AGAGGCATAA GCGGAGGAA CCGTGACAAA

121 : TGGGTATGCG AAGTCCGTGA ACCGATTCAT CAGCGTCGAG TCTGGCTCGG AACTTATCCG
     ***** **** * ** ***** * ** ** * * ***** *****
121 : TGGGTCTGCG AAGTCAGAGA ACCGACGCAC CAACGCCGCA TTTGGCTCGG GACTTATCCC

181 : ACGGCAGATA TGGCCGCACG TGCTCACGAC GTGGCGGTTT TTGCTCTGCG CGGGAGATCC
   ** ***** **** ** ** *** ***** ***** * ***** *****
181 : ACAGCAGATA TGGCAGCGCG TGCACACGAC GTGGCGGTTT TAGCTCTGCG TGGGAGATCC

241 : GCGTGTTTGA ATTTCTCCGA TTCTGCTTGG AGGTTGCCGG TGCCGGCATC CACTGATCCG
   ** ***** **** ** ***** ** * **** ***** ** ** *****
241 : GCATGTTTGA ATTTGCCGA CTCGCTTGG CGGCTTCCGG TGCCGGAATC CAATGATCCG

301 : GACACGATCA GCGGCACGGC GGCCGAAGCA GCGGAGATGT TCAGGCCGCC GGAGTTTAG-
   ** *** * * * ** *** ***** ***** * ***** *** *****
301 : GATGTGATAA GAAGAGTTGC GCGGAAGCT GCGGAGATGT TTAGGCCGGT GGA-TTTAGA

360 : TACAGGAATT ACGGTTTTAC CCTCAGC--C AG----- ----TGAGTT T-----
   * ***** ***** * * * ** ** ** *** *
360 : AAGTGAATT ACGGTTTTGC CTTGTGCGGG AGATGATGTG GATTTGGGT TTGTTTCGGG

397 : ----- ----GACA- ----- -CGT-CGGAT -----
   ** * ** ****
420 : TTCCGGCTCT GGTTCGGGAT CGGAGGAGAG GAATTCTTCT TCGTATGGAT TTGGAGACTA

409 : -GAAGGAGTC GCTGGAATGA TGATGAGGCT CGCGGAGGAG CCGTTGATGT CGCCGCCAAG
   **** **** * * ** ***** ** ***** * ** * **** ***** *
480 : CGAAGAAGTC TCAACGACGA TGATGAGACT CGCGGAGGGG CCACTAATGT CGCCGCCGCG

468 : ATCGTACAT- --TGATATGA ---ATACGAG TGTGTACGTG GACGAAGAAA TGTGTTACGA
   ***** ** ** **** *** * *** ** * ** ***** ***** **
540 : ATCGTATATG GAAGACATGA CTCCTACTAA TGTTTACACG GAAGAAGAGA TGTGTTATGA

522 : AGATTTGTCA CTTTGGAGTT AC-----TA A
   **** **** * ***** ** ** *
600 : AGATATGTCA TTGTGGAGTT ACAGATATTA A

```

Fig. 3-1

0046368

[GENETYX-MAC: Maximum Matching]
Date : 2003.03.03

+++++

Sequence 1 : DREB1A.aa
Size : 216
Matching Position : 1 - 216

Sequence 2 : DREB1B.aa
Size : 214
Matching Position : 1 - 214

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 85.78 [%]
Weight : -148

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
   *****      ****      ***** *****      ****
1 : MNSFSAFSEM FGSDYE---P QGGDYCPTLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG

61 : KKWCEVREPN KKTRIWLGTG QTAEMAARAH DVAALALRGR SACLNFADSA WRLRIPESTC
   *** ***** ***** ***** ***** ***** *****
58 : KKWCEVREPN KKTRIWLGTG QTAEMAARAH DVAALALRGR SACLNFADSA WRLRIPESTC

121 : AKDIQKAAAE AALAFQDEMC D-ATTDHGFD MEETLVEAIY TAEQSENAFY MHDEAMFEMP
   ***** ***** * * ** * * **** * * * * * * * * *
118 : AKDIQKAAAE AALAFQDETC DTTTNNHGLD MEETMVEAIY TPEQSEGAFY MDEETMFGMP

180 : SLLANMAEGM LLPLPSVQWN HNHEVDGDDD DVSLWSY-
   ** ***** *** ***** ** * * *****
178 : TLLDNMAEGM LLPPPSVQWN HNYDGEG-DG DVSLWSY*

```

+++++

Sequence 1 : DREB1A.aa
Size : 216
Matching Position : 1 - 216

Sequence 2 : DREB1C.aa
Size : 217
Matching Position : 1 - 217

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 86.70 [%]
Weight : -154

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
   ***** ***** ** ***** * ** ***** ***** ***** *****
1 : MNSFSAFSEM FGSDYESPVS SGGDYSPKLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG

61 : KKWCEVREPN KKTRIWLGTG QTAEMAARAH DVAALALRGR SACLNFADSA WRLRIPESTC
   ***** ***** ***** ***** ***** ***** ***** *****

```

Fig. 3-2

0046368

```

61 : K WVCELREPN KKTRIWLGT F QTAEMAARAH DVA AIALRGR SACLNFADSA WRLRIPESTC

121 : AKDIQKAAAE AALAFQDEMC DATTD-HGFD MEETLVEAIY TAEQSENAFY MHDEAMFEMP
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
121 : AKEIQKAAAE AALNFQDEMC HMTTDAHGLD MEETLVEAIY TPEQSQDAFY MDEEAMLGMS

180 : SLLANMAEGM LLPLPSVQWN HNHEVDGDDD DVSLWSY-
    *** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
181 : SLLDNMAEGM LLPSPSVQWN YNFDVEG-DD DVSLWSY*
  
```

+++++

```

Sequence 1      : DREB1A. aa
Size            : 216
Matching Position : 1 - 216

Sequence 2      : DREB1D. aa
Size            : 224
Matching Position : 1 - 224
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 65.04 [%]
Weight       : -56
  
```

```

1 : MNSF-SAF-- SEMFGSDYES SVSSGGDYIP TLASSCPKKP AGRKKFRETR HPIYRGVRRR
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSP KLASSCPKKR AGRKKFRETR HPIYRGVRRR

58 : NSGKWVCEVR EPNKKTRIWL GTFQTAEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    ***** * * * * * * * * * * * * * * * * * * * * * * * * * *
61 : NSGKWVCEVR EPNKKSRWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE

118 : STCAKDIQKA AAEALAFQD EMCDATTDHG FDMEETLVE- ----AIYTAE QSENAFYMH
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
121 : TTCPKIEQKA ASEAAAFQN ETTTEGSKTA AEAEAAAGEG VREGERRAE QNGGVFYMD

173 : EAMFEMPSLL ANMAEGMLLP LPSVQWNHNNH EVDGDDDDVS LWS--Y
    ** ** * * * * * * * * * * * * * * * * * * * * * * * * *
181 : EALLGMPNFF ENMAEGMLLP PPEVGWNHN- DFDG-VGDVS LWSFDE
  
```

+++++

```

Sequence 1      : DREB1A. aa
Size            : 216
Matching Position : 1 - 216

Sequence 2      : DREB1E. aa
Size            : 181
Matching Position : 1 - 181
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 45.87 [%]
Weight       : 32
  
```

Fig. 3-3

0046368

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
* ----- * * * * * * * * * * * * * * * *
1 : M----- -ENDDI-TVA EMKPKKRAGR RIFKETRHPI YRGVRRRDGD

61 : KVVCEVREPN KKTRIWLGTG QTAEMAARAH DVAALALRGR SACLNFAFSA WRLRIPESTC
***** * * * * * * * * * * * * * * * *
40 : KVVCEVREPI HQRVWLGTG PTADMAARAH DVAALALRGR SACLNFAFSA WRLPVFASD

121 : AKDIQKAAAE AALAFQDEMC DATTDHGFDM EETLVEAIYT AEQSENAFYM HDEAMFEMPS
* * * * * * * * * * * * * * * *
100 : PDTIRRTAAE AA----EM- -----FRP PE--FSTGIT VLPSASEFDT SDEGVAGMM

181 : LLANMAEGML LPLPSVQWNH NHEVD--GDD DDVSLWSY
** * * * * * * * * * *
145 : RLA-EEPLMS PPRSVIDMNT SVYVDEEMCY EDLSLWSY

```

+++++

```

Sequence 1      : DREB1A.aa
Size           : 216
Matching Position : 1 - 216

Sequence 2      : DREB1F.aa
Size           : 209
Matching Position : 1 - 209

```

Matching Condition.

```

Matches       : -1
Mismatches    : 1
Gaps          : 1
*NI          : 2

Matching      : 43.91 [%]
Weight       : 42

```

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
** ----- * * * * * * * * * * * * * * * *
1 : MN----- --NDDI-ILA EMRPKKRAGR RVFKETRHPI YRGIRRRNGD

61 : KVVCEVREPN KKTRIWLGTG QTAEMAARAH DVAALALRGR SACLNFAFSA WRLRIPESTC
***** * * * * * * * * * * * * * * * *
40 : KVVCEVREPT HQRRIWLGTG PTADMAARAH DVAALALRGR SACLNFAFSA WRLPVFASD

121 : AKDIQKAAAE AALAF--QDE MCDAT--TDH GFDMEETLVE AIYTAEQSE- -NAFYMHDEA
* * * * * * * * * * * * * * * *
100 : PDVIRRVAAE AAEMFRPVDL ESGITVLPCL GDDVDLGFSG GSGSGSGSEE RNSSSYGFGD

175 : MFEMPSLLAN MAEGMLLPLP -----SVQW NHNHEVDGDD DDVSLWS--Y
* * * * * * * * * * * * * * * *
160 : YEEVSTMMR LAEGLMSPP RSYMEDMTPT NVYTEEMCY EDMSLWSYRY

```

+++++

```

Sequence 1      : DREB1B.aa
Size           : 213
Matching Position : 1 - 213

Sequence 2      : DREB1C.aa
Size           : 217
Matching Position : 1 - 217

```

Fig. 3-4

0046368

Matching Condition.

```

Matches      :    -1
Mismatches   :     1
Gaps         :     1
*N+          :     2

Matching     :    86.18 [%]
Weight       :   -153

```

```

1 : MNSFSAFSEM FGSDYE---P QGGDYCPTLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG
   *****
1 : MNSFSAFSEM FGSDYESPV SGGDYSPKLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG

58 : KVVSEVREPN KKTRIWLGT QTAEMAARAH DVAALALRGR SACLNFA DSA WRLRIPESTC
    *** * ****
61 : KVVCELREPN KKTRIWLGT QTAEMAARAH DVAALALRGR SACLNFA DSA WRLRIPESTC

118 : AKDIQKAAAE AALAFQDETC DTTTTHGLD MEETMVEAIY TPEQSEGA FY MDEETMFGMP
    ** *****
121 : AKEIQKAAAE AALNFQDEMC HMTTDAHGLD MEETLVEAIY TPEQSQDA FY MDEEAMLGMS

178 : TLLDNMAEGM LLPPPSVQWN HNYDGE DGD VSLWSY-
    *****
181 : SLLDNMAEGM LLPPPSVQWN YNF DVEGDD VSLWSY*

```

+++++

```

Sequence 1      : DREB1B.aa
Size            :    213
Matching Position :      1 - 213

Sequence 2      : DREB1D.aa
Size            :    224
Matching Position :      1 - 224

```

Matching Condition.

```

Matches      :    -1
Mismatches   :     1
Gaps         :     1
*N+          :     2

Matching     :    65.93 [%]
Weight       :   -56

```

```

1 : MNSF-SAF-- SEMFGSDYEP QGGD---YCP TLATSCPKKP AGRKKFRETR HPIYRGVRQR
   ** * * * *
1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSP KLASSCPKGR AGRKKFRETR HPIYRGVRQR

55 : NSGKVVSEVR EPNKKTRIWL GTFQTAEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    *****
61 : NSGKVVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE

115 : STCAKDIQKA AAEALAFQD ETC DTTTTH GDMEE---T MVE--AIYTP EQSEGA FYMD
    ** * * * *
121 : TTCPEIKQKA ASEAMAFQN ET-TTEGSKT AAEAEAEAGE GVREGERRAE EQNGGV FYMD

170 : EETMFGMPTL LDNMAEGMLL PPPSVQWNHN YDGE DGDVS LWS--Y
    * * * *
180 : DEALLGMPNF FENMAEGMLL PPPEVGWNHN -DFDGV DVS LWSFDE

```

Fig. 3-5

0046368

+++++

Sequence 1 : DREB1B.aa
Size : 213
Matching Position : 1 - 213

Sequence 2 : DREB1E.aa
Size : 181
Matching Position : 1 - 181

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 44.95 [%]
Weight : 34

```

1 : MNSFSAFSEM FGSDYEPQGG DYCPATLASC PKKPAGRKKF RETRHPYRG VRQRNSGKWW
   *          * *          * *          * *          * *          * *
1 : M-----E NDDITVAEMK PKKRAGRRIF KETRHPYRG VRRRDGDKWW

61 : SEVREPNNKT RIWLGTFQTA EMAARAHDA ALALRGRSAC LNFADSAWRL RIPESTCAKD
    ***** * **** * ***** ***** *** ***** * **
43 : CEVREPIHQR RVWLGTYPTA DMAARAHDA VLALRGRSAC LNFSDSAWRL PVPASTDPDT

121 : IQKAAEAAL AFQDETCDDT TTNHGLDMEE TMVEAIYTP ESEGAFFYME ETMFGMPTLL
    * ***** * * *          * *          * *          * *
103 : IRRTAEEAAE MFRPPEFSTG IT-----VLPS ASE--FDTSD EGVAGMMMLL

181 : DNMAEGMLLP PPSVQWNHN- ---YDGE-GD GDVSLWSY
    ** * ** *          * *          * *****
147 : ---AEEPLMS PPRSVIDMNT SVYVDEEMCY EDLSLWSY

```

+++++

Sequence 1 : DREB1B.aa
Size : 213
Matching Position : 1 - 213

Sequence 2 : DREB1F.aa
Size : 209
Matching Position : 1 - 209

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 43.72 [%]
Weight : 43

```

1 : MNSFSAFSEM FGSDYEPQGG DYCPATLASC PKKPAGRKKF RETRHPYRG VRQRNSGKWW
   **          * *          * *          * *          * *          * *
1 : MN----- NDDIILAEMR PKKRAGRRVF KETRHPVYRG IRRRNGDKWW

61 : SEVREPNNKT RIWLGTFQTA EMAARAHDA ALALRGRSAC LNFADSAWRL RIPESTCAKD
    ***** * **** * ***** ***** ***** ***** ***
43 : CEVREPIHQR RVWLGTYPTA DMAARAHDA VLALRGRSAC LNFADSAWRL PVPESNDPDV

121 : IQKAAEAAL AF---QDETC DTTTNHGLD MEETMVEAIY TPEQSE---- --GAFYMDDE

```

Fig. 3-6

0046368

```

      *   *   *   *   *   *
103 : IRRVAAEAAE MFRPVDLESG ITVLPCAGDD VDLGFGSGSG SGSGSEERNS SSYGFGDYEE

      *   *   *   *   *   *
172 : TMFGMPTLLD NMAEGMLLP P-----SVQ WNHNYDGE-G DGDVSLWS-- Y
      *   *   *   *   *   *
163 : VSTTMMRL-- --AEGPLMSP PRSYMEDMTP TNVYTEEEMC YEDMSLWSYR Y
  
```

+++++

```

Sequence 1      : DREB1C.aa
Size            : 216
Matching Position : 1 - 216
  
```

```

Sequence 2      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 65.33 [%]
Weight            : -59
  
```

```

1 : MNSF-SAF-- SEMFGSDYES PVSSGGDYSP KLATSCPCKP AGRKKFRETR HPIYRGVRQR
  ** * * * * ** * *** ** *** ***** *****
1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSP KLASSCPKKR AGRKKFRETR HPIYRGVRQR

58 : NSGKWVCELR EPNKKTRIWL GTFQTAEMAA RAHDVAAIAL RGRSACLNFA DSAWRLRIPE
  ***** * ***** *** * ***** ** *****
61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE

118 : STCAKEIQKA AAEALNFQ- ---DEMCHMT TDAHGLDMEE TLVEAIYTP E QSQDAFYMDE
  ** ***** * *** ** * * * * *
121 : TTCPKEIQKA ASEAAAFQN ETTTEGSKTA AEAEAAAGEG VREGERRAE QNGGVFYMD

174 : EAMLGMSLL DNMAEGMLLP SPSVQWNYNF DVEGDDVSL WS--Y
  ** *** ***** * * * * * * * *
181 : EALLGMPNFF ENMAEGMLLP PPEVGWNHN- DFDGVDVSL WSFDE
  
```

+++++

```

Sequence 1      : DREB1C.aa
Size            : 216
Matching Position : 1 - 216
  
```

```

Sequence 2      : DREB1E.aa
Size            : 181
Matching Position : 1 - 181
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 43.24 [%]
Weight            : 42
  
```


Fig. 3-7

```

                                -0046368
1 : M-NSFSAFSE MFGSDYESPV SSGGDYSPKL ATSCPKKPAG RKKFRETRHP IYRGVRQRNS
   * * * * *
1 : MENDDITVAE M-----KPKKRAG RRIFKETRHP IYRGVRRRDG

60 : GKWVCELREP NKKTRIWLGT FQTAEMAARA HDVAAIALRG RSACLNFAADS AWRLRIPEST
   ***** * **** ** ***** **** ***** ** **** * **
39 : DKWVCEVREP IHQRRVWLGT YPTADMAARA HDVAVLALRG RSACLNFSDS AWRLPVPAST

120 : CAKEIQKAAA EALNFQDEM CHMTTDAHGL DMEETLVEAI YTPESQDAF YMDEEAMLGM
   * ** *** ** * * * * *
99 : DPTIRRTAA EAA----EM FRPPEFSTG-----ITVLPSASEF DTSDEGVAGM

180 : SLLDNMAEG MLLPSPSVQW NYNFDVEGD----DDVSLW SY
   * ** * * * * *
143 : MMRL---AEE PLMSPPRSYI DMNTSVYVDE EMCYEDLSLW SY

```

+++++

```

Sequence 1      : DREB1C.aa
Size            : 216
Matching Position : 1 - 216

```

```

Sequence 2      : DREB1F.aa
Size            : 209
Matching Position : 1 - 209

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

```

```

Matching         : 41.88 [%]
Weight           : 52

```

```

1 : MNSFSAFSEM FGSDYESPVS SGGDYSPKLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG
   ** * * * * *
1 : MN-----NDDIILA EMRPKKRAGR RVFKETRHPV YRGIRRRNGD

61 : KKWVCELREP NKKTRIWLGT FQTAEMAARA HDVAAIALRG RSACLNFAADS AWRLRIPESTC
   ***** * **** ** ***** **** ***** ** **** * **
40 : KKWVCEVREP IHQRRVWLGT YPTADMAARA HDVAVLALRG RSACLNFAADS AWRLPVPESTN

121 : AKEIQKAAA EALNF--QDE MCHMT-----TDAHGLDMEE TLVEAIYYPE --QSQDAFYM
   * *** ** * * * * *
100 : PDVIRRVAAE AAEMFRPVDL ESGITVLPCA GDDVDLGFGS GSGSGSGSEE RNSSSYGFGD

172 : DEEAMLGMS LLDNMAEGML LPSP-----SVQWNYNFD VEGDDVSLW S--Y
   ** * * * * *
160 : YEEVSTTMMR L----AEGPL MSPPRS YMED MTPTNVYTEE EMCYEDMSLW SYRY

```

+++++

```

Sequence 1      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224

```

```

Sequence 2      : DREB1E.aa
Size            : 181
Matching Position : 1 - 181

```

Matching Condition.

Fig. 3-8

0046368

```
Matches      : -1
Mismatch     : 1
Gaps         : 1
*N+          : 2

Matching     : 42.17 [%]
Weight       : 50
```

```
1 : MNPFYSTFPD SFLISDHRS PVSDSSECSP KLASSCPKKR AGRKKFRETR HPIYRGVRQR
   *      *
1 : MENDDIT--- ----- -VAEMKPKKR AGRRIFKETR HPIYRGVRRR

61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    ***** ** * ** ** ** ***** ** ***** ** ***** *
37 : DGDKWVCEVR EPIHQRRVWL GTYPTADMAA RAHDVAVLAL RGRSACLNFS DSAWRLPVPV

121 : TTCPKIEIQA ASEAAAFQN ETTTEGSKTA AEAEAAEGEG VREGERRAE QNGGVFYMD
    * * * * * ** * * * * * * * * * * * * * * * * * *
97 : STDPDTIRRT AAEEAEF-- ----- RPPEFSTGIT V---LPSASE -----FOTSD

181 : EALLGMPNFF ENMAEGMLLP PPEVGWNHND FDGV----- GDVSLWSFDE
    * ** * * * * * * * * * * * * * * *
137 : EGVAGM---M MRLAEPLMS PPSYIDMNT SVYVDEEMCY EDLSLWS--Y
```

+++++

```
Sequence 1      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224

Sequence 2      : DREB1F.aa
Size            : 209
Matching Position : 1 - 209
```

Matching Condition.

```
Matches      : -1
Mismatch     : 1
Gaps         : 1
*N+          : 2

Matching     : 42.13 [%]
Weight       : 49
```

```
1 : MNPFYSTFPD SFLISDHRS PVSDSSECSP KLASSCPKKR AGRKKFRETR HPIYRGVRQR
   **
1 : MN----- -NDDI LAEMRPKKR AGRRVFKETR HPVYRGIRRR

61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    * ***** ** ***** ** ** ** ***** ** ***** ** ***** **
37 : NGDKWVCEVR EPTHQRIWL GTYPTADMAA RAHDVAVLAL RGRSACLNFA DSAWRLPVPE

121 : TTCPKIEIQA ASEAAAFQN ETTTEG--SK TAAAEAAAG EGVREG-ERR AEEQNGGVFY
    * * * * * * * * * * * * * * * * * *
97 : SNPDVIRRV AAEEAEFMRP VDLESGITVL PCAGDDVDLG FGSGSGSGSG SEERNSSSYG

178 : MDDEALLGMP NFFENMAEGM LLPPP----E VGWNHN---- DFDGVGDVSL WSFDE
    * * * * * * * * * * * * * * *
157 : FGD--YEEVS TTMMRLAEGP LMSPPRSYME DMPTNVYTE EEMCYEDMSL WSYRY
```

+++++

Fig. 3-9

0046368

Sequence 1 : DREB1E.aa
Size : 181
Matching Position : 1 - 181

Sequence 2 : DREB1F.aa
Size : 209
Matching Position : 1 - 209

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 69.38 [%]
Weight : -71

```

1 : MENDDITVAE MKPKKRAGRR IFKETRHPIY RGVRRRDGDK WVCEVREPIH QRRVWLGTYP
  * **** * * ***** ***** * ** *** ** ***** * *** *****
1 : MNNDIILAE MRPKKRAGRR VFKETRHPVY RGIRRRNGDK WVCEVREPTH QRRVWLGTYP

61 : TADMAARAHD VAVLALRGRS ACLNFSDSAW RLPVPASTDP DTIRRTAAEA AEMFRPPEFS
  ***** ***** ***** ***** * ** * *** **** *****
61 : TADMAARAHD VAVLALRGRS ACLNFADSAW RLPVPESNDP DVIRRVAAEA AEMFRPVDLE

121 : TGITVLP--- -----SASEFD TS-----D EGVAGMMRL AEEPLMSPPR
  ***** * ** * * * **** ** *****
121 : SGITVLP CAG DDVDLGF GSG SGSGSGSEER NSSSYGFGDY EEVSTMMRL AEGPLMSPPR

157 : SY-IDM-NTS VYVDEEMCYE DLSLWS--Y
  ** ** * ** ***** * **** *
181 : SYMEDMTPTN VYTEEEMCYE DMSLWSYRY
  
```

Fig. 4-1

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+++++

Sequence 1 : DREB2A.nuc
 Size : 1008
 Matching Position : 1 - 1008

Sequence 2 : DREB2B.nuc
 Size : 993
 Matching Position : 1 - 993

Matching Condition.

Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2
 Matching : 63.40 [%]
 Weight : -222

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
    ***** ** * **** ** * ** *** ** ** *** ****
1 : ATGGCTGTAT ATGAACAAAC CGG----- AACCGAGCA- ----- GCCGAAGAAA

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA
    ***** * * *** * *** ** ***** * ** **** * *****
43 : AGGAAATCTA GGGCTCGAGC AGGTGGTTTA ACGGTGGCTG ATAGGCTAAA GAAGTGGAAA

121 : GAGTATAACG AGACCGTAGA AG----AAGT TTCTACCAAG AAGA----- ----GGAAA
    ***** **** *** ** ** ** * * * *** *** * ***
103 : GAGTACAACG AGATTGTTGA AGCTTCGGCT GTTAAAGAAG GAGAGAAACC GAAACGCAAA

166 : GTACCTGCGA AAGGGTCGAA GAAGGGTTGT ATGAAAGGTA AAGGAGGACC AGAGAATAGC
    ** ***** ***** *** ***** ***** **** ***** **
163 : GTTCCTGCGA AAGGGTCGAA GAAAGGTTGT ATGAAAGGTA AAGGAGGACC AGATAATTCT

226 : CGATGTAGTT TCAGAGGAGT TAGGCAAAGG ATTTGGGGTA AATGGGTTGC TGAGATCAGA
    * ***** * ***** *** ***** ***** ***** ***** **
223 : CACTGTAGTT TTAGAGGAGT TAGACAAAGG ATTTGGGGTA AATGGGTTGC AGAGATTCGA

286 : GAGCCTAATC GAGGTAGCAG GCTTTGGCTT GGTACTTTCC CTACTGCTCA AGAAGCTGCT
    ** ** ** *** * ** ***** ***** * **** ** * *****
283 : GAACCGAAAA TAGGAAC TAGTTCGGCTT GGTACTTTTC CTACCGCGGA AAAAGCTGCT

346 : TCTGCTTATG ATGAGGCTGC TAAAGCTATG TATGGTCCTT TGGCTCGTCT TAATTTCCCT
    ** ***** **** ** ** ** ***** ** ** * ***** **
343 : TCCGCTTATG ATGAAGCGGC TACCGCTATG TACGGTTCAT TGGCTCGTCT TAATTTCCCT

406 : CGGTCTGATG CGTCTGAGGT TACGAGTACC TCAAGTCAGT CTGAGGTGTG TACTGTTGAG
    * ***** ** ***** * *** ***** ** ***** * ***** **
403 : CAGTCTGTTG GGTCTGAGTT TACTAGTACG TCTAGTCAAT CTGAGGTGTG TACGGTTGAA

466 : A----- ---CTCCTGG TTGTGTTTAT GTGAAACAG AGGATCCAGA TTGTGAATCT
    * * *** * **** * ***** * * *** * ** *****
463 : AATAAGGCGG TTGTTTGTGG TGATGTTTGT GTGAAGCATG AAGATACTGA TTGTGAATCT

514 : AAACCCCT-- CTCCG---GT GGA--GTGGA GCCGATGTAT TGT----- --CTGGAGAA
    ** ** ** ** ** ** * ** * ** * ** * ** * ** * **
523 : AATCCATTTA GTCAGATTTT AGATGTTAGA GAAGA-GTCT TGTGGAACCA GGCCGGACAG

558 : TGGTGCGG-A AGAGATGAAG AGAGGTGTT- AAAGC-GGAT AAGCATTGGC TGAGCGAGTT
    * * *** ** ** *** * * * ** ** * ** * ** * **

```

Fig. 4-2

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```

582 : TTGCACGGTT GGACATCAAG ATATGAATTC TTCGCTGAAT TACGATTGTC TGTTAGAGTT

615 : TGAACATAAC TATTGGAGTG ATATTCTGAA AGAGAAAGAG AAACAGAAGG AGCAAGGGAT
    *** ** * ***** * * ** ** * ***** **** **** ** ** *
642 : TGAGCAGCAG TATTGGGGCC AAGTTTTGCA GGAGAAAGAG AAACCGAAGC AGGAA-GAAG

675 : TGTAGAAAC- CTGTCAGCAA CAACAGCAGG ATTCGCTATC TGTTGCAGAC TATGGTTGGC
    * *** ** ***** ** * *** * ** * * **** ** * ** **
701 : AGGAGATACA GCAACAGCAA CAGGAACAGC AACAGC-AAC AGCTGCA-AC -CGGATTGTC

734 : CCAATGATGT GGATCAGAGT --CACTTGA TTCTTCAGAC ATGTTTGATG TCGATGAG-C
    * ** * * ** * ** ***** ** ** ** * ** **** ** *
758 : TTACTGTTGC AGATTACGGT TGGCCTTGG- -TCTAATGAT ATTGTAAAT- --GATCAGAC

791 : TTCTACGTGA CCTAA--ATG GCGACGATGT GTTTCAGGC TTAAATCAGG ACCGGTACCC
    **** * ***** * ** **** * ** * * * * * *
813 : TTCTGGGAT CCTAATGAGT GCTTTGATAT TAATGAACTC CT---TGGAG ATTTGAA---

849 : GGGGAACAGT GTTGCCAACG GTTCATACAG GCCCGAGAGT CAACAAAGTG GTTTTGATCC
    **** ** *** * * * ** * ** * **** * ** * **
867 : --TGAACCTG GTCCCATCA G---AGCCAA GACCAA---- -AACCACGTA AAT----TCT

909 : GCTACAAAGC CTCAACTACG GAATACCTCC GTTTCAGCTC GAGGGAAAGG ATGGTAATGG
    * * * * * * ** * * * ** * **** * ** * * **** *
913 : GGT----- --AGTTATG ATTTGCATCC GCTTCATCTC GAGCCACACG ATGGTCACG-

969 : ATTCTTCGAC GACTTGAGTT ACTTGATCT GGAGAACTAA
    *** * * ***** *** ** * *
962 : --AGTTCAAT GGTTGAGTT -----CTCT GGATATTGA
  
```

+++++

```

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008
  
```

```

Sequence 2      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 55.22 [%]
Weight       : -8
  
```

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAG- AAACAGAACA CAAATTGATA CATCGAGGAA
    ** ** * ***** * **** * ** ** ****
1 : AT-GCCGT-- ----- CGGAGATTGT TGACAGGAA- -AAG--GAAG TCTCGTGGAA

60 : AAGGAAATCT AGAAGTAGAG GTGACGGTAC TACTGTGGCT GAGAGATTAA AGAGATGGAA
    * ** * * ** * *** * ** * * * * * * ****
44 : CACGAGATGT AGCTG-AGAT TCTAAGGCAA TGGAGAGAGT ---ACAATGA GCAGATTGAG

120 : AGAGTATAAC GAGACCGTAG AAGAAGTTTC TACCAAGAAG AGGAAAG-TA CCTGCGAAAG
    ** ** * * ** * * * ** * * ** ***** *** * ****
100 : GCAGAATCTT G-TATCGATG GTGGTG-GTC CAAAATCAAT CCGAAAGCCT CCTCCAAAAG
  
```

Fig. 4-3

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```

179 : GGTCCAAGAA GGGTTGTATG AAAGGTAAAG GAGGACCAGA GAATAGCCGA TGTAGTTTCA
    * **** *** ***** ***** * ***** ** * *** * *
158 : GTTCGAGGAA GGGTTGTATG AAAGGTAAAG GTGGACCTGA AAACGGGATT TGTACTATA

239 : GAGGAGTTAG GCAAAGGATT TGGGGTAAAT GGGTTGCTGA GATCAGAGAG CCTAATCGAG
    ***** ** **** ***** ***** ***** * *** ** * ***
218 : GAGGAGTTAG ACAGAGGAGA TGGGGTAAAT GGGTTGCTGA GATCCGTGAG CCAGACGGAG

299 : GTAGCAGGCT TTGGCTTGGT ACTTTCCTTA CTGCTCAAGA AGCTGCTTCT GCTTATGATG
    ** *** * ***** *** ***** * * * * ** ***** * ***** *
278 : GTGCTAGGTT GTGGCTCGGT ACTTTCCTTA GTTCATATGA AGCTGCATTG GCTTATGACG

359 : AGGCTGCTAA AGCTATGTAT GGTCTTTTGG CTCGTCTTAA T-TTCCC--- -----TC
    **** ** * ***** *** ***** * * * * ** * * ***** **
338 : AGGCGGCCAA AGCTATATAT GTTCAGTCTG CCAGACTCAA TCTTCCCGAG ATCACAAATC

407 : GGTCTGATGC GTCTGAGG-- -TTACGAGTA CCTCAAG-TC AGTCTGAGGT GTGTACTGTT
    * *** * * * *** * * * * * ** * * * * * * * * * *
398 : GCTCTTCTTC GACTGCTGCC ACTGCCACTG TGTCAGGCTC GGT-TACTGC ATTTTCTGAT

463 : GAGACTCCTG GTTGTGTTCA TGTGAAAACA GAGG---ATC CAGATTGTGA ATCTAAACCC
    ** ** * ***** * ** * * *** * * * * ** * * ** *
457 : GAATCTGAAG TTTGTGCACG TGAGGATACA AATGCAAGTT CAGGTTTTG- GTC---AGGT

520 : TTCTCCGGTG GAGTGGAGCC GATG--TATT GTCTGGAGAA TGGTGGCGAA GAGATGAAGA
    * * * * * * * * * * * * * * * * * * * * * * * *
513 : GAAACTAGAG GATTGTAG-C GATGAATATG TTCTCTTAGA TAGTTCTCAG TGTATTAA-A

578 : GAGGTGTAA AGCGGATAAG CATTGGCTGA GCGAGTTTGA ACATAACTAT TGGAGTGATA
    **** * * * * * * * * * * * * * * * * * * * * * *
571 : GAGGAGCTGA A-AGGAAAAG -AGGAAGTGA GGA---AGA ACATAACT-T GGCTGTTGGT

638 : TTCTGAAAGA GAAAGAGAAA CAGAAGGAGC AAGGGATTGT AGAAACCTG- -TCAGCAACA
    ** *** ** * * * * * * * * * * * * * * * * * * *
625 : TTTGGAATTG GACAG-GACT C-GAAAAGG- --GAGACTTT GGATGCTTGG TTGATGGGAA

696 : ACAGCAGGAT TCGCTATCTG TTGCAGACTA TGGT-TGGCC CAA-----TG ATGTGGATCA
    * *** * * * * * * * * * * * * * * * * * * * *
680 : ATGGCAATGA ACAAGAACCA TTG--GAGTT TGGTGTGGAT GAAACGTTTG ATATTAAT--

750 : GAGTCACTTG GATTCTTCA- -GACATGTTT GATGTCGATG AGCTTCTACG TGACCTAAAT
    *** * * * * * * * * * * * * * * * * * * * * *
736 : GAGCTATTGG GTATATTAAA CGACAACAAT G-TGTC--TG ---GTC-AAG AGAC---AAT

808 : GGCG-ACGAT GTGTTTGCAG GCTTAAATCA GGACCGGTAC CCGGGGAACA GTGTTGCCAA
    * * * * * * * * * * * * * * * * * * * * * *
786 : GCAGTATCAA GTGGATAGAC ACCCAAAT-- -TTCAGTTAC C----AAACG CAGTTTCCAA

867 : CGGTTTCATAC AGGCCCGAGA G--TCAACAA AGTGGTTTTG ATCCGCTACA AAGCCTCAAC
    *** ** * * * * * * * * * * * * * * * * * * *
839 : --ATTCTAAC TTGCTCGGGA GCCTCAACCC TATGGAGAT- -TGCTCAACC AGGAGTTGAT

925 : TACGGAATAC CTCCGTTTCA GCTC---GA- --GGGAAAGG ATGGTAATGG ATT-----
    ** *** * * * * * * * * * * * * * * * * * *
895 : TATGGATGTC CTTATGTGCA GCCCAGTGAT ATGGAGAACT ATGGTATTGA TTAGACCAT

972 : -----CTTCG ACGA-CTTGA GTT-----AC TTGGATCT-- --GGAGA--- -----
    *** * * * * * * * * * * * * * * * * *
955 : CGCAGGTTCA ATGATCTTGA CATACAGGAC TTGGATTTTG GAGGAGACAA AGATGTTTCAAT

```

Fig. 4-4

1004 : -----AC-T AA
 * * * *
 1015 : GGATCTACAT AA

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+++++

Sequence 1 : DREB2A.nuc
 Size : 1008
 Matching Position : 1 - 1008

Sequence 2 : DREB2D.nuc
 Size : 621
 Matching Position : 1 - 621

Matching Condition.

Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2

 Matching : 44.17 [%]
 Weight : 226

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
   ***                                     * * * * *
1 : ATG-----TCATCC ATAGAG----

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA
     * * * * * * * * * * * * * * * * * * * * * *
16 : -----CCA AAAGTA---A TGATGGT--- --TGGTGCT- ----AATAA- -----GAA-

121 : GAGTATAACG AGACCGTAGA AGAAGTTTCT ACCAAGAAGA GGAAAGTACC TGCGAAAGGG
      * * * * * * * * * * * * * * * * * * * * *
48 : ----ACAACG A-ACCGT--- -CCAAG--- -C T-----AGT

181 : TCGAAGAAGG GTTGTATGAA AGGTAAAGGA GGACCAGAGA ATAGCCGATG TAGTTTCAGA
     **** * * * * * * * * * * * * * * * * * * * *
70 : TCGAGGAAAG GTTGTATGAG AGGAAAAGGT GGACCCGATA ACGCGTCTTG CACTTACAAA

241 : GGAGTTAGGC AAAGGATTTG GGGTAAATGG GTTGCTGAGA TCAGAGAGCC TAATCGAGGT
     ** * * * * * * * * * * * * * * * * * * * *
130 : GGTGTTAGAC AACGCACTTG GGGCAAATGG GTCGCTGAGA TCCGCGAGCC TAACCGAGG-

301 : AGC-AGGCTT TGGCTTGGA CTTCCCTAC TGCTCAAGAA GCTGCTTCTG CTTATGATGA
     *** * * * * * * * * * * * * * * * * * * *
189 : AGCTCGTCTT TGGCTCGGTA CTTTCGACAC CTCCCGTGAA GCTGCCTTGG CTTATGACTC

360 : GGCTGCT--A AAGCTATGTA TGGTCCTTTG GCTCGTCTTA ATTTCCCTCG GTCTGATGCG
     ** * * * * * * * * * * * * * * * * * *
249 : CGCAGCTCGT AAGC--TCTA TGGGCCTGAG GCTCATCTCA ACCTCCCT--

418 : TCTGAGGTTA CGAGTACCTC AAGTCAGTCT GAGGTGTGTA CTGTTGAGAC TCCTGGTTGT
     **** * * * * * * * * * * * * * * * *
295 : -----GAGT-CCTT AA----- GAAGT---TA C-----CCT-----

478 : GTTCATGTGA AAACAGAGGA TCCAGATTGT GAATCTAAAC CCTTCTCCGG TGGAGTGGAG
     * * * * * * * * * * * * * * * *
316 : -----A AAACGGCG-- -TCGTCTCCGG CG-----T

538 : CCGATGTATT GTCTGGAGAA TGGTGCGGAA GAGATGAAGA GAGGTGTTAA AGCGGATAAG
     ** * * * * * * * * * * * * * * *
338 : CCCA----- GACTACACCA AGCAGC---- -AACA CCGGTG---- -GAAAAAG
  
```

Fig. 4-5

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```

598 : CATTGGCTGA GCGAGTTTGA ACATAACTAT TGGAGTGATA TTCTGAAAGA GAAAGAGAAA
      ** ** * **** * ***          * * ***      *** *   ** ****
375 : CA---GC--A GCGACTCTGA -----GT CGCCGTG--- TTC----ATC CAACGAGA--

658 : CAGAAGGAGC AAGGGATTGT AGAAACCTGT CAGCAACAAC AGCAGGATTG GCTATCTGTT
      * * *      *** ** **          ** ** ****  * ****
413 : ---TGTCATC A-----TGT GGAAGAGTG- -----AC AG-AGGA--- GATATC----

718 : GCAGACTATG GTTGGCCCAA TGATGTGGAT CAGAGTCACT TGGATTCTTC AGACATGTTT
      *** *** ** * ** ***** * * *
447 : ----- --ATG-GGAG CATATAAACG TGGATT-TGC CG-----GT

778 : GATGTCGATG AGCTTCTACG TGACCTAAAT GGCGACGATG TGTTCGAGG CTTAAATCAG
      *** **** * ****          * * ** ** ** *      * * ** ***
477 : AATG--GATG A--TTCT--- --TCAATAT GG---GAAG -----AAG CTACAAT---

838 : GACCGGTACC CGGGGAACAG TGTGCGCAAC GGTTCATACA GGCCCGAGAG TCAACAAAGT
      ** **      ***          ** *** ***** * **      * * *
513 : -GTCGTTA-- ---GGA----- --TTCCATG GGTTCATGAA GG----- --AGATAAT

898 : GGTTCGATC CGCTACAAAG CCTCAACTAC GGAATACCTC CGTTTCAGCT CGAGGGAAG
      * * ** ** * *          **** *      **** * *      *
550 : GATATTTCTC GGTT----- -----TGATACTTG TATTTCCGGT -----G

958 : GATGGTAATG GATTCTTCGA CGACTTGAG- TTACTTGGAT CTGGAGAACT AA
      * *      *****          * *** * ** *** **      * *
584 : GCT----- -ATTCT---- --AATTGGGA TTCCTTTCAT TCCCCACTTT GA

```

+++++

```

Sequence 1          : DREB2A.nuc
Size                : 1008
Matching Position   : 1 - 1008

```

```

Sequence 2          : DREB2E.nuc
Size                : 735
Matching Position   : 1 - 735

```

Matching Condition.

```

Matches           : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 49.90 [%]
Weight           : 128

```

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAAT-----T GATACATCGA
    **** *      * ** ***          *** ** ***** * *      * * *
1 : ATGGAA---A AGGA--AGAT AACGGATCGA AACAGAGCTC CTCTGCTTCT GTTGATCTCT

56 : GGAAAAGGAA ATCTAGAAGT AGAGGTGACG GTACTACTGT GGCTGAGAGA TTAAAGAGAT
    ** ***      **** *** ** * *      * ** ** * **      *** *****
56 : CGAGAAG--- ---ACGAAGA AGA-GTG--G TTGAGCCAGT GGAAGCGACG TTACAGAGAT

116 : GGAAAGAGTA TAACGAGACC GTAGAAGAAG TTTCTACCAA GA-AGAGGAA AGTACCTGCG
    **      ***          ***** * * * * **      * *      * *
107 : GG----- ----GAG--- ---GAAGAAG GAT-TGGCGA GAGCTCGTAG GGTTCAGGCC

175 : AAAGGGTCCA AGAAGGGTTG TATGAAAGGT AAAGGAGGAC CAGAGAATAG CCGATGTAGT

```


Fig. 4-6

```

                                -0010181
148 : *****
      AAAGGTTCGA AGAAAGGTTG TATGAGAGGA AAAGGTGGAC CAGAGAATCC TGTTTGTCGG

235 : TTCAGAGGAG TTAGGCAAAG GATTGGGGT AAATGGGTTG CTGAGATCAG AGAGCCTAAT
      ** ***** * ** * ***** * ***** ***** * ** **
208 : TTTAGAGGTG TTCGACAAAG GGTGTTGGGG AAATGGGTTG CTGAGATACG TGAACC----

295 : CGAGGTAGCA GGCTTTGGCT TGGTACTTTC CCTACTGCTC AAGAAGCTGC TTCTGCTTAT
      ** ** * * **** * * *** * * * ** * ** ***
264 : --AGTGAG-- ----TCACCG TGGTGCAAAC TCTAGT-CGT AGTAAACGGC TTTGGCTTGG

355 : GATG-AGGCT GCTAAAGCTA TGTATGGTCC TTTGGCTCGT CTTAATTTCC CTCGGTCTGA
      * * *** ** **** * * * * *****
315 : CACGTTTGCT ACTGCAGCT- --GAAGCTGC TTTGGCT--- -----

414 : TGCCTCTGAG GTTACGAGTA CCTCAAGTCA GTCTGAGGTG TGTACTGTTG AGACTCCTGG
      * * * * * * * * * * **** * * * *
349 : TACGACAGA- GCTGCTAGT- -----GTCA ----- TGTAC----- GGAC-CCT--

474 : TTGTGTTTCT GTGAAAACAG AGGATCCAGA TTGTGAATCT AAACCCTTCT CCGGTGGAGT
      ** * **** ** * *** ** **** ** *
383 : -----AT G----- ----CCAG- --GT-----T AAA---TTTC CCGGAAGATT

534 : GGAGCCGATG TATTGTCTGG AGAATGGTGC GGAAGAGATG AAGA-GAGGT GTTAAAGCGG
      * * ** ** * **** * * * * * * * * * *
410 : TGGG----- --TG---GG GGAA----- GGAAGA-AGG ACGAGGAGGC GGAAAGTTGC

593 : ATAAGC-ATT GGCTGAGCGA GTTTGAACAT AAC---TATT GGAGTGATAT TCTGAAAGAG
      * ** *** ** ** * * **** * * * * * * * *
451 : GGAGGCTATT GGTG---GA AACT-AACAA AGCCGGTAAT GGCCTGAT-- --TGAACGG

649 : AAAGAGAAAC AGAAGGAGCA AGGGATTGTA GAAACCTGTC AGCAACAACA GCAGGATTCC
      ** * * * * * * * * * * **** * * **** * * **
503 : AAGGTGGAAG AGA-----CT A-----TGTA G----- -TCTACAA-- --TGAAGACG

709 : CTATCTGTTG CAGACTATGG TTGGCCCAAT GATGTGGATC AGAGTCACTT GGATTCTTCA
      **** * * * * * * * * * * * * * * *
539 : CTAT----- ----TGAGC TTGGCC--AT GA-----C A-AG--ACTC AGAATCCT--

769 : GACATGTTTG ATGTCGATGA GCTTCTACGT GACCTAAATG GCGACGATGT GTTTCAGGCG
      *** ** ** **** * ** ** * * * *
574 : ---ATGACTG AT---AATGA AAT---AGT GAAC----- --CCA--- --GCAG--

829 : TTAAATCAGG ACCGGTACCC GGGGAACAGT GTTGCCAACG GTTCATACAG GCCCGAGAGT
      * * * * * * * * * * **** * * *
605 : TGAAATCAG- --AGGAA--- -GGTTACAGC TATG--ATCG ATTCAAATTG G-----

889 : CAACAAAGTG GTTTTGATCC GCTACAAAGC CTCAACTACG GAATACCTCC GTTTCAGCTC
      * * * * * * * * * * * * * * *
647 : --ATAACGGA TTGTG---- --TATAA--- -TGAACCTC- --AAAGCTCC AGTT-ATCAC

949 : GAGGGAAAGG ATGGTAATGG ATTCTTCGAC GACTTGAGTT ACTTGGATCT GGAGAACTAA
      ***** * * * * * * * * * * * *
691 : CAGGGA---G GTGG-ATTCG ATTC---AT ATTTTGAGTA TTTGAGAT-- ----TCTAG

```

+++++

```

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008

```

Fig. 4-7

0010181

Sequence 2 : DREB2F.nuc
 Size : 834
 Matching Position : 1 - 834

Matching Condition.

Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2
 Matching : 48.48 [%]
 Weight : 158

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
    ****                      ****                      ***
1 : ATGG-----AGAA-----ATC-----

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA
    ***                      ** * ** *** * *****
12 : -----ATC-----CTC A---ATGAAA CA-ATGGAA-

121 : GAGTATAACG AGACCGTAGA AGAAGTTTCT ACCAAGAAGA GGAAAGTACC TCGGAAAGGG
    *** * ** ***
33 : -----GAAGGGTCC TGC-----

181 : TCGAAGAAGG GTTGTATGAA AGGTAAAGGA GGACCAGAGA ATAGCCGATG TAGTTTCAGA
    *** ***** ** *** * * * * * * * *
45 : TCG-----GGGTAAAGGC GGTCCACAAA ACGCTCTTTG TCAGTACCGT

241 : GGAGTTAGGC AAAGGATTTG GGGTAAATGG GTTGCTGAGA TCAGAGAGCC TAA-TCGAGG
    ***** ** ***** ** ***** ***** **
88 : GGAGTCAGGC AAAGGACTTG GGGCAAATGG GTGGCTGAGA TCAGAGAGCC CAAGAAGAGG

300 : TAGC-AGGCT TTGGCTTGGT ACTTTCCCTA CTGCTCAAGA AGCTGCTTCT GCTTATGATG
    * * * * * ***** ** * * * * * * *
148 : --GCAAGACT TTGGCTTGGC TCTTTCGCTA CAGCTGAAGA AGCAGCTATG GCTTATGATG

359 : AGGCTGCTT AAAGCTATGT ATGGTCCTTT GGCTCGTCTT AATTTCCTCT GGTCTGATGC
    ***** * * * * * * * * * * * * * * *
206 : AGGCTGCTT GAAAC--TCT ATGGGCACGA CGCATACCTC AACTTACCTC -ATCTTCAGC

417 : GTCTGAGGTT ACGAGTACCT CAAGTCAGTC TGAGGTGTGT ACTGT-TGAG ACTCCTGGTT
    * * * * * * * * * * * * * * *
263 : G-----GAAT ACAAG-ACCT ----TC--TC TGAG----TA ACTCTCAGAG GTTC--AAAT

476 : GTGTTTCATG TAAACAGAG GATCCAGATT GTGAATCTAA ACCCTTCTCC GGTGGAGTG-
    * * * * * * * * * * * * * * *
305 : GGTACCT-- ----TCA-AG GA---AGTTT AT--ATCTAT GTTTCCTTCA TGTGGTATGC

535 : GAGCCGATGT ATTGTCTGGA GAATGGTGCG GAAGAGATGA AGAGAGGTGT TAAAGCGGAT
    * * * * * * * * * * * * * * *
353 : TAAACG-TGA ATGCTC---A GCCTAGTGT CACATAATCC AGCAAAGACT AGAAGAACTC

595 : AAGCATTGGC TGAGCGAGTT TGAACATAA- -CTATTGGAG T-GATATTCT GAAAGAGAAA
    *** * * * * * * * * * * * * * * *
409 : AAGAA--AAC TG---GACTT TTATCTCAAT CCTATTCTTC TAGTCTTCC TCCACCGAAT

652 : GAGAAAC-AG AAGGAGC--A AGGGAT-TGT AGA--AACCT GTCAGCAACA -ACAGCAGGA
    * * * * * * * * * * * * * * *
464 : CAAAACTAA TACTAGCTTT CTTGATGAGA AGACCAGCAA GGGAGAAACA GACAATATG-
```

Fig. 4-8

0010181

```

705 : TTCGCTATCT GTTG--CAG- ----ACTATG GTTGGCCCAA TGA-TGTGGA TC-AGAGTCA
      *** * * * * ***      * * * * * *** * * * * ***
523 : TTCG-AAGGT GGTGATCAGA AGAAACCAGA GATCGACC-- TGACCGAGTT TCTTCAGCAA

756 : CTTGGATTCT TCAGACATG- -TTTGATGTC GA-----TG AGCT-TCTAC GTGACCTAAA
      ** *** *** * * ***      *** * * * * ** * * * * * *** * *
580 : CTAGGAATCT TGAAGGATGA AAATGAAGCA GAACCAAGTG AGGTAGCAGA GTGTCATTCC

807 : TGGCGACGAT -GTGTTTGCA GGCTTAAATC AGGACCGGTA CCCGGGGAAC AGTG-TTGCC
      * * * * * * * * * * * * * * * * * * * * * * * * *
640 : CCTCCACCAT GGAACGAGCA AGAAGAAA-C TGA--AGTC CTTTCAGAAC TGAGAATTTC

865 : AACGGTTCAT A-CAGGCCCG AGAGTCAACA AAGTGGTTTT GATCCGCTAC AAAGC--CTC
      * * * * * * * * * * * * * * * * * * * * * * * * *
697 : AGCTG-GGAT ACCCTGATCG AGATGCCAAG AAGTG----- AAACCACAAC TATGCAATTT

922 : AACTACGGAA TACCTCCGTT TCAGCT-CGA GGGAAAGGAT GGTAATGGAT TCTTC---GA
      *** * * * * * * * * * * * * * * * * * * * * * *
751 : GACTCCAGCA -ACTTCGG-- -AAGCTATGA TTTTGAGGAT G---ATGTAT CCTTCCCTTC

978 : CGACTTGAGT TACT-TGGAT CTGGAGAACT AA
      * * * * * * * * * * * * * * * *
804 : CATCTGGGAC TACTACGGAA GCTTAG-ATT GA

```

+++++

```

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 47.08 [%]
Weight       : 149

```

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
   ****
1 : ATGG-----

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA
    : ----- ** * **
    : -----AA G-----AA

121 : GAGTATAACG AGACCGTAGA AGAAGTTTCT ACCAAGAAGA GGAAAGTACC TGCGAAAGGG
     *** * * * * * * * * * * * * * * * *
10 : GAGCA----- --ACC----- --TCCG GCCAAGAA-A CGAA---ACA TGGGGA--GA

181 : TCGAAGAAGG GTTGTATGAA AGGTAAAGGA GGACCAGAGA ATAGCCGATG TAGTTTCAGA
     * * * * * * * * * * * * * * * * *
46 : TCTAGAAAAG GTTGCATGAA AGGTAAAGGC GGTCCAGAGA ACGCCACGTG TACTTTCCGT

241 : GGAGTTAGGC AAAGGATTTG GGGTAAATGG GTTGCTGAGA TCAGAGAGCC TAATCGAGGT
     ***** ** * * * ***** ** * * * ***** ** * *

```

Fig. 4-9

0010181

```

106 : GGAGTTAGGC AACGGACTTG GGGTAAATGG GTGGCTGAGA TCCGTGAGCC TAACCGTGGG

301 : AGCAGGCTTT GGCTTGGTAC TTTCCCTACT GCTCAAGAAG CTGCTTCTGC TTATGATGAG
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
166 : ACTCGTCTCT GGCTCGGCAC GTTAAATACC TCGGTCGAGG CCGCCATGGC TTACGATGAA

361 : GCTGCTAAAG CTATGTATGG TCCTTTGGCT CGTCTTAATT TCCCTCGGT- CTGATGCGTC
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
226 : GCCGCTAAGA AACTCTATGG ACACGAGGCT AAACCTAA-- ---CTTGGTG CACCCACAAC

420 : TGAGGTTACG AGTACCTCAA GTCAGTCTGA GGTGTGTACT GTTGAGACTC CTGGTTGTGT
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
281 : AACACAACA AGTA---GTA GTGA-ACAGA AACTTGTCTT TTTCTGGCCA CGGTCGGGT

480 : TCATG----T GAAAACAGAG GATCCAGATT GTGAAT---C TAAACCT-- TCT---CCGG
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
337 : TCTTGGGCTT ATAATAAGAA GCTCGATATG GTTCATGGGT TGGACCTTGG TCTCGGCCAG

528 : TGGAGTGGAG C-CGATG-TA TTGTCTGGAG A-ATGGTGGC GAAGAGATGA AGAGAGGTGT
    *** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
397 : GCAAGTTGTT CACGAGGTTC TTGCTCAGAG AGATCGAGTT TTCTACAAGA AGA-TGATGA

585 : TAAAGCGGAT AAGC-AT-TG GCTGAGCGAG TTTGAACATA ACTATTGGAG TGATATTCTG
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
456 : TCATAGTCAT AATCGATGTT CGTCTTCAAG -TGGTTCGAA TCT-TTGTG -GTTATTACC

643 : AAAGAGAAAG AGAAACAGAA GGAGCAAGGG ATTGTAGA-- ----AACCTG TCA--GCAAC
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
513 : TAA-ACAAAG TGATTCACAA -GATCAAGAG ACCGTTAATG CTACGACTAG TTATGGCGGT

695 : AACAGCAGGA TTCGCTAT-- ----CTGTTG CAGACTATGG TTGGCCCAAT GATGTGGATC
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
571 : GAAGGCCGTG GTGGCTCTAC GTTAAACGTTT TCGACCAATT TGAAACCAAA GAATTTGATG

749 : AG--AGTCAC TTGATTCTT CA---GA--- ----CATGT TTGATGT--- -CGATGAGCT
    ** ** * * * * * * * * * * * * * * * * * * * * * * * * * *
631 : AGTCAGAATT ATGGATTATA CAATGGAGCT TGGTCTAGGT TTCTTGTGGG GCAAGAAAAG

792 : TCTACGTGAC CT-AAATGGC GACGATGTGT TTGCAGGCTT AAATCAGGAC CGGTACCCGG
    *** ** * * * * * * * * * * * * * * * * * * * * * * * * *
691 : AAGACGGAAC ATGACGTGTC ATCGTCGTGT GGATCGTCGG ACAACAAGGA GAGTATGTTG

851 : GGAAC-AG-T GTTGCCAACG GTTCATACA- GGCCCGAGAG TCAACAAAGT GGTTTTGATC
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
751 : GTTCCTAGTT GCGGCGGAGA GAGGATGCAT AGGCCG-GAG TTGGAAGAGC GAACAGGATA

908 : CGCTACAAAG CCTCAACTAC GGAATACCTC CGTTTCAG-- --CTCGA-GG GAAAGGATGG
    ** * * * * * * * * * * * * * * * * * * * * * * * * * *
810 : TTTGGAATG GATGATCTTT TGGAGATTGA TGATTAGGT TTGTTGATTG GCAAAAATGG

963 : -----T AATGGATTCT TCGACGACTT --GAGTTACT TGGATCTGGA GAACTAA
    *** * * * * * * * * * * * * * * * * * * * * * * * * *
870 : AGATTCAAG AATTGGTGTG GTGAAGAGTT TCAACATCCA TGAATTG-- GTTCTGA
  
```

+++++

```

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008
  
```

```

Sequence 2      : DREB2H.nuc
  
```

Fig. 4-10

0010181

Size : 534
Matching Position : 1 - 534

Matching Condition.

Matches : -1
Mismatch : 1
Gaps : 1
*N+ : 2

Matching : 39.41 [%]
Weight : 304

```

1 : ATG-GCAGTT TATGATCAGA GTGGAGATAG AAACAGAAACA CAAATTGATA CATCGAGGAA
   *** *** * * ** * * * * ***** * * ** * **
1 : ATGCCCAGGA AACG-GAAGT CTCGTG----- ----GAACA CGAGATGTAG CTGAGATTCT

60 : AAGGAAATCT AGA-AGTAGA GGTGACGGTA CTA CTGTGGC TGAGAGATTA AAGAGATGGA
   ***** *** ***** * *** * * ** * *** ***** * ** **
51 : AAGGAAATGG AGAGAGTACA -ATGA--GCA -GACCGAGGC ----AGATTCTTG-CATCGA

119 : AAGAGTATAA CGAGACCGTA GAAGAAGTTT CTACCAAGAA GAGGAAAGTA CCTGCCAAAG
   * * ** * ** ***** ** * * * *** * ***
102 : TGGTG----- -----GTG GTTCAA---- -AACCAATCC GA--AAGGCT CCTCCAAAC

179 : GGTCCAAGAA GGGTTGTATG AAAGGTAAAG GAGGACCAGA GAATAGCCGA TGTAGTTTCA
   * **** *** ***** * ***** ** *** * *** * *
143 : GTTCGAGGAA GGGTTGTATG AAAGGTAAAG GTGGACCTGA AAATGGGATT TGTGACTATA

239 : GAGGAGTTAG GCAAAGGATT TGGGGTAAAT GGGTTGCTGA GATCAGAGAG CCTAATCGAG
   ***** ** **** ***** ***** ***** * *** ** ****
203 : CAGGAGTTAG ACAGAGGACA TGGGGTAAAT GGGTTGCTGA GATCCGTGAG CCAGGCCGAG

299 : GTAGCAGGCT TTGGCTTGGT ACTTTCCCTA CTGCTCAAGA AGCTGCTTCT GCTTATGATG
   ** * * * ***** *** ***** * * * * ***** * *****
263 : GTGCTAAGTT ATGGCTCGGT ACTTTCTCTA GTTCATATGA AGCTGCATTG GCTTATGATG

359 : AGGCTGCTAA AGCTATGTAT GGTCCCTTGG CTCGTCTTAA TTTCCCTCGG TCTGATGCGT
   ***** * ** ***** *** ** ** **
323 : AGGCTTCCAA AGCTAT----- -----TTA- -----CGG TC-----AGT

419 : CTGAGGTTAC GAGTACCTCA AGTCAGTCTG AGGTGTGTAC TGTGAGACT CCTGGTTGTG
   *** * * * * * * * * * * * * * * * *
350 : CTG----- -----CCCG ACTCAATCT- -----TCCAC TGCTGCCAC- -----TGTG

479 : TTCATGTGAA AACAGAGGAT CCAGATTGTG AATCTAAACC CTTCTCCGGT GGAGTGGAGC
   * *** * * * * **
384 : T----- ---CAGGCT C--GGT--- ---AC- -----

539 : CGATGTATTG TCTGGAGAAT GGTGCGGAAG AGATGAAGAG AGGTGTTAAA GCGGATAAGC
   ** *** *** *****
398 : ---TGCAATT TCT----- -GATGAA---

599 : ATTGGCTGAG CGAGTTTGAA CATAACTATT GGAGTGATAT TCTGAAAGAG AAAGAGAAAC
   **** ***** * * * * *
414 : ---TCTGA- --AGTTG-- ----- --TGCACGTG A-----

659 : AGAAGGAGCA AGGGATTGTA GAAACCTGTC AGCAACAACA GCAGGATTGG CTATCTGTTG
   **** *
434 : ----- --GGAT----- -ACAAAT GCA-----

```

Fig. 4-11

0010181

```

719 : CAGACTATGG TTGGCCCAAT GATGTGGATC AGAGTCACTT GGATTCTTCA GACATGTTTG
      *** * *** **          * * ** *** ** **          ****
447 : -AGA-TCTGG TT----- ----TTGGTC AGA-TCTCT- ---AACTTC- -----

779 : ATGTCGATGA GCTTCTACGT GACCTAAATG GCGACGATGT GTTTGCAGGC TTAAATCAGG
      ***          * * ** *****          **** **
477 : ---TCG---- -----CAT TTCCAAATG ----- TTAAGTC---

839 : ACCGGTACCC GGGGAACAGT GTTGCCAACG GTTCATACAG GCCCGAGAGT CAACAAAGTG
      ** *          *** * ***          **
500 : -----CAAT -----AAC- -TGCAT----- -TG

899 : GTTTTGATCC GCTACAAAGC CTCAACTACG GAATACCTCC GTTTCAGCTC GAGGGAAAGG
      ***          ***          **          ***
514 : GTT-----AAG- ----- --TT----- --GG-----

959 : ATGGTAATGG ATTCTTCGAC GACTTGAGTT ACTTGATCT GGAGAACTAA
      * ***          ****
525 : -----GCGTT -----ACTAG

```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

```

```

Sequence 2      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 54.32 [%]
Weight       : 12

```

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
  ** ** **          *** * * * * ** * * * * * * * * * *
1 : AT-GCCGT-- ----- CGG-AGATTG TTGAC-AGGA AAAGGAAGTC TCG---TGGA

61 : GCAGGTGGTT TAACGGTGCC TGATAGGCTA AAGAAGTGGA AAGAGTACAA CG---AGATT
  ** * * *          ** ** *** * *** * * * * * * * * * * *
43 : ACACGAGAT- -----GTAGC TGAGATTCTA AGGCAATGGA GAGAGTACAA TGAGCAGATT

118 : GTTGAAGCTT CGGCTGTAA AGAAGGAG-- -AGAAACCGA AACGCAAAGT TCCTGCGAAA
  * * * * * * * * * * * * * * * * * * * * * * * * * *
97 : GAGGCAGAAT CTTGTATCGA TGGTGGTGGT CCAAAATCAA TCCGAAAGCC TCCTCAAAA

175 : GGGTCGAAGA AAGGTTGTAT GAAGGGTAAA GGAGGACCAG ATAATTCTCA CTGTAGTTTT
  ** **** ** * * * * * * * * * * * * * * * * * * * *
157 : GGTTCGAGGA AGGGTTGTAT GAAAGGTAAA GGTGGACCTG AAAACGGGAT TTGTGACTAT

235 : AGAGGAGTTA GACAAAGGAT TTGGGGTAAA TGGGTTGCAG AGATTGAGA ACCGAAAATA
  * * * * * * * * * * * * * * * * * * * * * * * * * *
217 : AGAGGAGTTA GACAGAGGAG ATGGGGTAAA TGGGTTGCTG AGATCCGTGA GCCAGACGGA

295 : GGAAC TAGAC TTTGGCTTGG TACTTTTCCT ACCGCGGAAA AAGCTGCTTC CGCTTATGAT

```

Fig. 4-12

```

                                -0010181
277 : ** **** * ***** ** ***** * * * * ***** * *****
      GGTGCTAGGT TGTGGCTCGG TACITTTCTCC AGTTCATATG AAGCTGCATT GGCTTATGAC

355 : GAAGCGGCTA CCGCTATGTA CGGTTTCATTG GCTCGTCTTA A-CTTCCC-- --TCA-----
      ** ***** * ***** ** *** * ** * ** * * ***** ***
337 : GAGGCGGCCA AAGCTATATA TGGTCAGTCT GCCAGACTCA ATCTTCCCGA GATCACAAAT

405 : ----- -GTCTG---- -----TT GGGTCTG--- AGTTTACTAG TACGTCTAGT
      * *** * * * * * * * * * * * * * * * * * * * * * *
397 : CGCTCTTCTT CCACTGCTGC CACTGCCACT GTGTCAGGCT CGGTTACTGC ATTTTCTGAT

439 : CAATCTGAGG TGTGTACGGT TGAAAATAAG GCGGTTGTTT GTGGTGATGT TTGTGTGAAG
      ***** * * * * * * * * * * * * * * * * * * * * *
457 : GAATCTGAAG TTTGTGCACG TGAGGATACA AATGCAAGTT CAGGTTTGG TCAGGTGAAA

499 : CATGAAGATA CTGATTGTGA ATCTAATCCA TT---TAG-- -TCAG---AT TTTAGA----
      * ** * * * * * * * * * * * * * * * * * * * * * *
517 : CTAGAGGATT GTAGCGATGA ATATGTTCTC TTAGATAGTT CTCAGTGTAT TAAAGAGGAG

546 : -TGTTA-GAG AAGA-GTCTT GTG----GAA CCAGGCCGGA CAGTTG--CA CGG--TTGGA
      ** * * * * * * * * * * * * * * * * * * * * * *
577 : CTGAAAGGAA AAGAGGAAGT GAGGGAAGAA CATAACTTGG CTGTTGGTTT TGAATTGGA

595 : CA----TCAA GATATGAATT CTTGCGTGAA TTACGATTGG CTGTTA---G AGTTTGAGC-
      ** * * * * * * * * * * * * * * * * * * * * * *
637 : CAGGACTCGA -AAAGGGAGA CTT---TGGA TGCTTGGTTG ATGGGAAATG GCAATGAACA

647 : AGCAGTATTG GGGCCAAGTT TTGCAGGAGA AAGAGAAACC GAAGCAGGAA GAAGAGGAGA
      ** * * * * * * * * * * * * * * * * * * * * * *
693 : AGAACCATTG GAG-TTGGT GTGGATGAAA CGTTTGATAT TAATGAGCTA -TTGGGTATA

707 : TACAGCAACA GCAACAGGAA CAG-CAACAG -CAA--CAGC TGCAACCGGA TTTGCTTACT
      * * * * * * * * * * * * * * * * * * * * * *
751 : TTAAACGACA ACAATGTGTC TGGTCAAGAG ACAATGCAGT ATCAAGTGGA TAGAC--AC-

763 : GTTGCAAGT ACGGTTGGCC TTGGTCTAAT G-ATATTGTA AATGATCAGA CTT-CTTGGG
      ** *** * *** * * * * * * * * * * * * * * * *
808 : ---CCAAATT TCAGTT---- ---ACCAAC GCAGTTTCCA AAT--TCTAA CTGCTCGGG

821 : ATCCTAATGA GTGCTTTGAT ATTAATGAAC TCCTTGGAGA TTTGAATGAA CCTGGTCCC
      * * * * * * * * * * * * * * * * * * * * * *
856 : AGCCTCA--A CCCTATGGAG ATTGCTCAA- --CCAGGAG- -TTG-ATTAT GGATGTCCTT

881 : ATCAGAGCCA AGACCAAAAC CACGTA-AAT TCTGGTAGTT ATGATTGCA T--CCGCTTC
      ** * * * * * * * * * * * * * * * * * * * * *
908 : AT--GTGC-- AGCCAGTGA TATGGAGAAC TATGGTATTG ATTTAGACCA TCGCAGGTTT

938 : ----ATCTCG AGCCACACGA --TGG--TCA CGAG--TTCA ATGGTTTGAG TTCTCTGGA-
      ***** * * * * * * * * * * * * * * * * *
964 : AATGATCTTG ACATACAGGA CTTGGATTTT GGAGGAGACA AAGAT----G TTC-ATGGAT

987 : -TATTTGA
      ** * *
1019 : CTACATAA

```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

```

Fig. 4-13

0010181

```

Sequence 2      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

Matching Condition.

Matches        : -1
Mismatch      : 1
Gaps           : 1
*N+            : 2

Matching       : 43.12 [%]
Weight         : 231

 1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
    *** *      * * * * * * * * * * * * * * * *
 1 : ATGTC-----ATC C---ATAGAG C-----CA AAAGTAA-----

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGA AAGAGTACAA CGAGATTGTT
    * ***** ** * * * * * * * * * * * * * * *
26 : --TGATGGTT ---GGT-GC TAAT----- AAGAA-----ACAA CGA-ACCGTC

121 : GAAGCTTCGG CTGTAAAGA AGGAGAGAAA CCGAAACGCA AAGTTCCTGC GAAAGGGTCG
     ***** ** * * * * * * * * * * * * * * *
61 : CAAGCT-----AGT-----TCG

181 : AAGAAAGGTT GTATGAAGGG TAAAGGAGGA CCAGATAATT CTCACTGTAG TTTTAGAGGA
    * ***** ** * * * * * * * * * * * * * * *
73 : AGGAAAGGTT GTATGAGAG AAAAGGTGGA CCCGATAACG CGTCTTGAC TTACAAAGGT

241 : GTTAGACAAA GGATTTGGGG TAAATGGGTT GCAGAGATTC GAGAACCGAA AATAGGAACT
    ***** * * ***** * * * * * * * * * * * *
133 : GTTAGACAA GCACCTGGGG CAAATGGGTC GCTGAGATCC GCGAGCCTAA CCGAGGAGCT

301 : AGACTTTGGC TTGGTACTTT TCCTACCGCG GAAAAAGCTG CTTCCGCTTA TGATGAAGCG
    * ***** * * * * * * * * * * * * * * * *
193 : CGTCTTTGGC TCGGTACCTT CGACACCTCC CGTGAAGCTG CTTGGCTTA TGACTCCGCA

361 : GCTACCGCTA TGTACGGTTC ATTGGCTCGT CTTAACTTCC CTCAGTCTGT TGGGTCTGAG
    *** * * * * * * * * * * * * * * * * * * *
253 : GCTCGTAAGC TCTATGGGCC TGAGGCTCAT CTCAACCTCC CTGAGTC-CT TAAG---AAG

421 : TT-TACTAGT ACGTCTAGTC AATCTGAGGT GTGTACGGTT GAAAATAAGG CGGTTGTTTG
    ** *** *** * * * * * * * * * * * * * * *
309 : TTACCCTAAA ACGGC--GTC -GTCTCCGGC GTCCAGACT --ACACCAAG CAGCAACACC

480 : TGGTGATGTT TGTGTGAAGC ATGAAGATAC TGATTGTGAA TCTAATCCAT -TTAGTCAGA
    * ** * * * * * * * * * * * * * * * *
364 : GGTGGAAA-- ----AAGC A-GCAG---- CGACTCTGAG TC---GCCGT GTTCATCCAA

539 : TTTTAGATGT TAGAGAAGAG TCTTGTGGAA CCAGGCCGGA CAGTTGCACG GTTGGACATC
    ***** * ** ***** * ** *** * * * *
408 : --CGAGATGT CA-----TCATGTGGAA ----GAGTGA CAG-----AG G--AGATATC

599 : AAGATATGAA TTCTTCGCTG AATTACGATT TGCTGTTAGA GTTTGAGCAG CAGTATTGGG
    * * * * * * * * * * * * * * * * * *
447 : ATGGGA-GCA T-----ATA AACGTGGATT TGCCGGTAAT GGATG-----ATTCTT---

659 : GCCAAGTTTT GCAGGAGAAA GAGAAACCGA AGCAGGAAGA AGAGGAGATA CAGCAACAGC
    *** * * * * * * * * * *
491 : --CAA--TAT G-----GGAAGA-----

```


Fig. 4-14

0010181

```

719 : AACAGGAACA GCAACAGCAA CAGCTGCAAC CGGATTTGCT TACTGTTGCA GATTACGGTT
      **** ***          *** *      *** ** *
504 : ----- -AGCTACAA- ----- ---TGTCG-- --TTA-GGAT

779 : GGCCTTGGTC TAATGATATT GTAAATGATC AGACTTCTTG GGATCCTAAT GAGTGCTTTG
      ** *** * **** * * ** * * * **** * *      ****
524 : TTCCATGGGT TCATGA---A GGAGATAATG ATATTCTCG G----- -TTTG

839 : ATATTAATGA ACTCCTTGGA GATTTGAATG AACCTGGTCC CCATCAGAGC CAAGACCAAA
      ***          ****      ***      * **
566 : ATA----- ---CTTG-- TATTT----- ---CCGG-- -----

899 : ACCACGTAAA TTCTGGTAGT TATGATTTGC ATCCGCTTCA TCTCGAGCCA CACGATGGTC
      *** * * * ** * * * * **** * ** **      *
582 : ----- ---TGGCTAT TCTAATTGGG ATTCCTTTCA T-TC---CC- -----C

959 : ACGAGTTCAA TGGTTTGAGT TCTCTGGATA TTTGA
      **                      *****
615 : AC----- -TTGA

```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

```

```

Sequence 2      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 49.22 [%]
Weight            : 140

```

```

1 : ATGG---CTG TATATGAACA AACCGGAACC GAGCAGCCGA AGAAAAGGAA ATCTAGGGCT
   **** * * ** *** * ** *** **** ** * * * ** **
1 : ATGGAAGGAGG AAGAT-AACG GATCGAAACA GAGC-TCCTC TGCTTCTG-- TTGTA-TCCT

58 : CGAGCAGGTG GTTTAACGGT GGCTGATAGG CTAAAGAAGT GGAAAGAGTA CAACGAGATT
     **** * * * ** ** ** ** * * **** * * **** * * **
56 : CGAG-AAGAC GAAGAAGAGT GGTGTA---G C-----CAGT GGA----- -AGCGACGT

118 : GTTGAAGCTT CGGCTGTTAA AGAAGGA--- GAGAAACCGA AACGCAAAGT TCCTGCGAAA
      ** * * * * * ***** * ** * * ** * ** **
99 : ACAGA--GAT GGGAGG---A AGAAGGATTG GCGAGAGC-- -TCGTAGGT TCAAGCCAAA

175 : GGGTCGAAGA AAGGTTGTAT GAAGGGTAAA GGAGGACCAG ATAATTCTCA CTGTAGTTTT
     ** ***** ***** ** ** *** ** ***** * ** ** *** * **
151 : GGTTCGAAGA AAGGTTGTAT GAGAGGAAAA GGTGGACCAG AGAATCCTGT TTGTCGGTTT

235 : AGAGGAGTTA GACAAAGGAT TTGGGGTAAA TGGGTTGCAG AGATTCGAGA ACC-----
     ***** ** ***** * ***** ** ***** * **** ** **
211 : AGAGGTGTTC GACAAAGGAT TTGGGGGAAA TGGGTTGCTG AGATACGTGA ACCAGTGAGT

288 : -----G AAAA---TAG --GAACATA-- -GACTTTGGC TTGGTACTTT TCCTACCGCG
      * *** ** * * ** * ***** **** ** ** * **** **

```

Fig. 4-15

-0010181

```

271 : CACCGTGGTG CAAACTCTAG TCGTAGTAA CGGCTTTGGC TTGGCACGTT TGCTACTGCA

331 : GAAAAAGCTG CTTCCGCTTA TGATGAAGCG GCTACCGCTA TGTACGGTTC ATTGGCTCGT
      * ***** ** *** **** * * ***** * * ** *
331 : GCTGAAGCTG CTTTGGCTTA CGACAGAGCT GCTAGTGTCA TGTACGGACC CTATGCCAGG

391 : CTTAACCTCC CTCAGTCTGT TGGGTCTGAG TTTACTAGTA CGTCTAGTCA ATCTGAGGTG
      * ** **** * * * * ***** * * ** * ** * *
391 : TTAAATTTCC CGGAAGAT-T TGGGTGGGG -----AAGGA -----AG--A A-----

451 : TGTACGGTTG AAAATAAGGC GGTGTGTTGT GGTGATGTTT GTGTGAAGCA TGAAGATACT
      * *** * **** ** * *** * *** * ** * ** *
429 : -GGACG----- -AGGAGGC GG----- -AAAGTT- -----CG GGAGGCTATT

511 : GATTGTGAAT CTAATCCATT TAGTCAGATT TTAGATGTGA GAGAAGAGTC TTGTGGAACC
      * *** *** **** ** ** * * ** *** * ** * ** *
461 : GGTG-GAAA CTAA--CA-- AAGCCGG--- -TA-ATG--- -----GCGTG AT-TGAAA--

571 : AGGCCGGACA GTTGACCGGT TGGACATCAA GA-TATGAAT TCTTCGCTGA ATTACGATT
      **** * **** ** ** **** * *** * * ** *
500 : ----CGGA-- -----AGG TGGA---AAA GACTATGTAG TCTAC----A ATGAAGA--C

630 : GCTGTTAGAG TTTGAGCAGC AGTATTGGGG CCAAGTTTTG CAGGAGAAAG AGAAACCGAA
      *** ***** ** ** *** ** * *** **** ** *
538 : GCT----- ATTGAGC--- ----TT--GG CCA-----TG -ACAAGACTC AGAATCCTAT

690 : GCAGGAAGAA GAGGAGATAC AGCAACAGCA ACAGGAACAG CAACAGCAAC AGCTGCAACC
      * **** * ** ** **** ***** ** ** *
576 : G----- --ACTGATAA TGAAATAG-- ---TGAAC-- --CCAGCA-- --GTGAAATC

750 : GGATTGCTT ACTGTTGCAG ATTACGGTTG GCCTTGGTCT AATGATATTG TAAATGATCA
      ** * ** **** * ** *****
612 : AGA----- ----GGAAG GTTACAG--- -----CT -----ATGATC-

810 : GACTTCTTGG GATCCTAATG AGTGCTTTGA TATTAATGAA CTCCTTGGAG ATTGGAATGA
      *** * ** ** ** * ** * ** * ** *
635 : ----- GATTCAAA-- ----TTGA T-----AA CGGATTGTTG --TATAATGA

870 : ACCTGGTCCC CATCAGAGCC AAGACCAAAA CCACGTAAAT TCTGGTAGTT ATGATTTGCA
      **** **** **
669 : ACCT----- ----CAAA- ----- -GC-

930 : TCCGCTTCAT CTCGAGCCAC ACGATGGTCA CGAGTTCAAT GGTTTGAGTT CTCTGGATAT
      *** ** * * * * * * ** *** ** * ** *
679 : TCCAGTT-AT CACCAGGGA- --GGTGGATT CGA-TTC-AT ATTTTGAGTA TTTCAGAT-T

990 : TTGA
      *
732 : CTAG

```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

```

```

Sequence 2      : DREB2F.nuc
Size            : 834
Matching Position : 1 - 834

```

Matching Condition.

Fig. 4-16

0010181

Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2
 Matching : 48.46 [%]
 Weight : 138

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
    ****                      *** **      ***      ***
1 : ATGG----- -----A AGA AA---TCATC -----CTC--

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGA AAGAGTACAA CGAGATTGTT
    * * ***      ****
18 : -----A ATGAA-----ACAA -----

121 : GAAGCTTCGG CTGTTAAAGA AGGAGAGAAA CCGAAACGCA AAGTTCCTGC GAAAGGGTCG
    ** ** **      * * * * *      ***
28 : -----TG-----GA AG-----A AGGGTCCTGC -----TCG

181 : AAGAAAGGTT GTATGAAGGG TAAAGGAGGA CCAGATAATT CTCACTGTAG TTTTAGAGGA
    *** * * * * * * * * * * * * * * * * * * * *
48 : -----GGG TAAAGGCGGT CCACAAAACG CTCCTTGTCA GTACCGTGGA

241 : GTTAGACAAA GGATTGGGG TAAATGGGTT GCAGAGATTC GAGAACCGAA -AATAGGAAC
    ** ** * * * * * * * * * * * * * * * * * * * *
91 : GTCAGGCAAA GGAATTGGGG CAAATGGGTG GCTGAGATCA GAGAGCCCAA GAAGAGG-GC

300 : TAGACTTTGG CTTGGTACTT TTCCTACCGC GGAAAAAGCT GCTTCCGCTT ATGATGAAGC
    * * * * * * * * * * * * * * * * * * * * * *
150 : AAGACTTTGG CTTGGCTCTT TCGCTACAGC TGAAGAAGCA GCTATGGCTT ATGATGAGGC

360 : GGCTACCGCT ATGTACGGTT CATTGGCTCG TCTTAAGTTC CCTCAGTCTG TTGGGTCTGA
    ** * * * * * * * * * * * * * * * * * *
210 : TGCCTTGAAA CTCTATGGGC ACGACGCATA CCTCAACTTA CCTCA-TCTT CAGCG-----

420 : GTTACTAGT ACGTCT---A GTCAATCT-- GAGGTGTGTA CGGTGAAAA TAAGGCGGTT
    * * * * * * * * * * * * * * * * * * * *
264 : GAATACAAGA CCTTCTCTGA GTAACCTCTA GAGGTTCAAA TGGGT-ACCT TCA--AGGAA

475 : GTTGTGGTG ATGTTTGTGT GAAGCATGAA G-ATACTGAT TGTGAAT-CT AATCCATTTA
    * * * * * * * * * * * * * * * * * * * *
321 : GTTTAT---- ATCTATGTTT CCTTCATGTG GTATGCTAAA CGTGAATGCT CAGCC---TA

533 : GTCAGATTTT AGATGTTAGA GAAGAGTCTT GTGGAAC-CA GG----CCGG ACAGTT---G
    ** ** * * * * * * * * * * * * * * * *
374 : GT----GTTT ACATAATCCA GCAAAGACTA GAAGAACTCA AGAAAAGTGG ACTTTTATCT

585 : CACGGTTGGA CATCAAGATA TGAATTCTTC GCTGAATTAC GATTGCTGT TAGAGT--TT
    ** * * * * * * * * * * * * * * * * * *
430 : CAATCCTATT CTTCTAGTTC T---TCCTCC ACCGAATCAA AAATAATAC TAGCTTTCTT

643 : GAGCAGCAGT ATTGGGGCCA AGTTTTGCAG GAGAAAGAGA AACCGAAGCA GGAAGAAGAG
    ** ** * * * * * * * * * * * * * * * *
487 : GATGAGAAG- ACCAG---CA AG-----G GAGAAACAGA CA-ATATGTT CGAAG--GTG

703 : GAGATACAGC AACAGCAACA G---GAACAG CAACAGCAAC AGCTGCAACC GGATTTGCTT
    * * * * * * * * * * * * * * * * * *
533 : GTGAT-CAGA AGAAACCAGA GATCGACCTG ACCGAGTTTC TTCAGCAACT AGGAATCTTG
  
```

Fig. 4-17

0010181

```

760 : ACTGTTGCAG ATTACGGTTG GCCTTGGTCT AATGATATTG TAAATGATCA GACTTCTTGG
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
592 : AAGGATGAAA ATGAAG---- --CAGAACCA AGTGAGGTAG CAGAGTGTCA TTCCCTCCA

820 : GATCCTAATG AGTGCTTTGA TATTAATGAA CTCCTTGGAG ATTTG---AA TGAACCTGG-
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
646 : CCATGGAACG AGCAAGAAGA AACT--GGAA GTCCTTTCAG AACTGAGAAT TTCAGCTGGG

876 : -TCCCC--AT C-AGA-GCCA AG-ACCAAAA CCACGTAAAT TCTGGTAGTT ATGATTTGCA
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
704 : ATACCCTGAT CGAGATGCCA AGAAGTGAAA CCAC---AAC TATGCAA--T TTGA-CTCCA

930 : TCCGCTTC-- -ATCT-CGAG CCACACGATG --GT---CAC GAGTTCAATG GTTTGAGTTC
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
758 : GCAACTTCGG AAGCTATGAT TTTGAGGATG ATGTATCCTT CCCTTCCAT- CTGGGACTAC

981 : TCTGGA---- TA-TTTGA
      * * * * * * * * * *
817 : TACGGAAGCT TAGATTGA
  
```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993
  
```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 48.32 [%]
Weight            : 163
  
```

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCG-
    **** * * * * * * * * * * * * * * * * * * * * * * * * * *
1 : ATGGAAGAAAG AGCAAC-CTC CGG--CCAAG AAACGAAACA TGGGGAGATC TAGAAAAGGT

60 : AGCAGGTGGT TTAACGGTGG --CTGATA-- GGCTAAAGAA -----GTGG AAAGAGTACA
    *** * * * * * * * * * * * * * * * * * * * * * * * * * *
58 : TGCATGAAAG GTAAAGGCGG TCCAGAGAAC GCCACGTGTA CTTTCCGTGG AGTTAG-GCA

110 : ACGAGATTGT TGAAGCTTCG GCTGTTAAAG A-AGGAGAGA AACCGAAACG CAAAGTTCCT
    *** *** * * * * * * * * * * * * * * * * * * * * * * * *
117 : ACGGACTTGG GGTAAT--G GGTGGCTGAG ATCCGTGAG- --CCTAACCG --TGGGACTC

169 : GCGAAAGGGT CGAAGAAAGG TTGTATGAAG GGTAAGGAG GACCAGATAA TTCTACTGT
    * * * * * * * * * * * * * * * * * * * * * * * * * * *
170 : GTCTCTGGCT CG--GCACGT TTAATACCTC GGT---CGAG GCCGCCATGG CTTACGATGA

229 : AG--TTTTAG AGGAGTTA-- GACAAAGGAT TTGGGGTAAA TGGGTTGCAG AGA-TTCGAG
    ** * * * * * * * * * * * * * * * * * * * * * * * * * *
225 : AGCCGCTAAG AAACCTCTATG GACACGAGGC TAAACTCAAC TTGG-TGCAC CCACAACAAC

284 : AACCGAAAT AGGAACTAGA CTTTGGCTTG GTACTTTTCC TACCGCGGAA AAAGCTGCTT
    *** * * * * * * * * * * * * * * * * * * * * * * * * * *
284 : AACACAAGT A-GTAGTGA CAGAAACTT- GTCTTTTCTT GCCCACGG-G TCGGGTCTT
  
```

Fig. 4-18

0010181

```

344 : CCGCTTATGA TGAAGCGGCT ACCGCTATGT ACGGTTTCATT GGCTCG-TCT TAAC TTCCT
      ***** * * *** ** ** ***** ** * * * *
341 : GGGCTTATAA T-AAGAAGCT --CGATAT-- --GGTTCATG GGTTCGACCT TGGTCTCGGC

403 : CAGTC-TGTT GGGTCTGAGT TTACTAGTAC GTCTAGTCAA TCTGAGGTGT GTACGGTTGA
      *** * *** * *** ** * * * * ** * ** * * *** **
394 : CAGGCAAGTT GTTCACGAGG TT-CTTGCTC AGAGAG---A TC-GAGTTT CTAC--AAGA

462 : AAATAAGGCG GTTGTGTTGT GT-GATGTTT GT-GTGAAGC ATGAAGATAC --TGATTGTG
      * * * * * * * * * * ***** ** * *** ** * * * *
447 : AGATGATGAT CATAGTCATA ATCGATGTTT GTCTTCAAGT GGTTCGAATC TTTGTTGGTT

518 : A--ATCTAAT C-CATTTAGT CAGATTTTAG ATGTTAGAGA AGAGTCTTG- TGAACACAGG
      * * **** * * * * * ** * ** ***** * * * * * *
507 : ATTACCTAAA CAAAGTGATT CACA----AG AT-CAAGAGA CCGTTAATGC TACGACTAGT

574 : CCGGACAGTT GCA--CGGTT GGACATCAAG ATATGAATTC TTCGCTGAAT T-----
      * * * * * * ***** * * * * * * * * * * ***** *** *
562 : TATGGC-GGT GAAGGCGGTG GTGGCTCTAC GT-TAACGTT TTCGACCAAT TTGAAACCAA

623 : ACGATTTGCT G-----T TAGAGTTTGA GCAGCAGTAT TGGGGCCAAG TTT-TGCAGG
      * ***** * * * * * * * * * * ** * * * * * * * * *
620 : AGAATTTGAT GAGTCAGAAT TATGGATTAT ACAATGGAGC TTGGTCTAGG TTTCTTGTTG

674 : AGAAAGAGAA ACCGAAGCAG GAAGAAGAGG AGATACAGCA ACAGCAACAG GAACAGC-AA
      * **** * * * * * * * * * * * * * * * * * * * * *
680 : GGCAAGA-AA A--GAAGACG GAACATGACG TG-----TCA TCGTCGTGTG GATCGTCGGA

733 : CAGCAACAGC TGCAACCGGA TTTGCTTACT GTTGACAGATT ACGGTTGGCC TTGGTCTAAT
      ** *** * * * * * * * * * * ** * * * * * * * *
732 : CAACAAGGAG AGTATGTTG- GTTCCTAGTT GCGGCGGAGA GAGGAT-GCA TAGGCC----

793 : GATATTGTAA ATGATCAGAC TTCTTGGGAT CCTAATGAGT GCTTTGATAT TAATGAACCT
      * *** ** * * * * * * * * * * ** * * * * * * * *
786 : GGAGTTGGAA --GAGCGAAC -----AGGAT ----AT---- --TTGGAAT GGATGATCT-

853 : CTTGGAGATT TGAATGAACC TGGTCCCAT CAGAGCCAAG ACCAAAACCA CGTAAATTCT
      ***** * * * * * * * * * * * * * * * * * *
828 : TTTGGAGATT --GATGATT AGGT-----T TGTG--ATT GGCAAAA--A TGGAGATT--

913 : GGTAGTTATG ATTTGCATCC GCTTCATCTC GAGCCACAGC ATGGTCACGA GTTCAATGGT
      * * * * * * * * * * * * * * * * * * * *
875 : -----TCAAG AATTG----- ----GTGTT GTG----AAG A--GTTTCAA CATCCATGGA

973 : TTGAGTTCTC TGGATATTG A
      * **** * *
914 : ATTGGTTC-- -----TG A

```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

Matches : -1

Fig. 4-19

0010181

Mismatches : 1
Gaps : 1
#N+ : 2
Matching : 39.24 [%]
Weight : 295

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
   **                                     *** * ** ** **** ** * * * **
1 : AT----- ----- --GCCCAGGA AACGGAAGTC TCG---TGGA

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGGG AAGAGTACAA CG---AGATT
   ** * * * ** ** ** *** * *** * *** **** * **** * * **
28 : ACACGAGAT- ----GTAGC TGAGATTCTA AGGAAATGGA GAGAGTACAA TGAGCAGACC

118 : GTTGAAGCTT C-GGC--TGT TAAAGAAGGA GAGAAACCGA AACGCAAAGT TCCTGCGAAA
   * * ** ** * ** * * * ** **** * ** ** * **** * ***
82 : GAGGCAGATT CTTGCATCGA TGGTGGTGGT TCAAAACCAA TCCGAAAGGC TCCTCCAAAA

175 : GGGTCGAAGA AAGGTTGTAT GAAGGGTAAA GGAGGACCAG ATAATTCTCA CTGTAGTTTT
   * **** ** * **** * ** * **** * * **** * * **** * *
142 : CGTTCGAGGA AGGTTGTAT GAAAGGTAAA GGTGGACCTG AAAATGGGAT TTGTGACTAT

235 : AGAGGAGTTA GACAAAGGAT TTGGGGTAAA TGGGTTGCAG AGATTGAGA ACCGAAAATA
   * **** * ** * **** * **** * **** * **** * **** * **
202 : ACAGGAGTTA GACAGAGGAC ATGGGGTAAA TGGGTTGCTG AGATCCGTGA GCCAGGCCGA

295 : GGAAGTAGAC TTTGGCTTGG TACTTTTCCT ACCGCGGAAA AAGCTGCTTC CGCTTATGAT
   ** *** * **** * ** * **** * ** * * * **** * * **** *
262 : GGTGCTAAGT TATGGCTCGG TACTTTCTCT AGTTCATATG AAGCTGCATT GGCTTATGAT

355 : GAAGCGGCTA CCGCTATGTA CGGTTTCATTG GCTCGTCTTA ACTTCCCTCA GTCTGTGGG
   ** ** * * **** * ** * **** * **** * **** *
322 : GAGGCTTCCA AAGCTATTTA CGG----- -----TCA GTCTG-----

415 : TCTGAGTTTA CTAGTACGTC TAGTCAATCT GAGGTGTGTA CGGTTGAAAA TAAGGCGGTT
   * * **** * * *
353 : -----CCC GACTCAATCT -----TC C-----

475 : GTTTGTGGTG ATGTTTGTGT GAAGCATGAA GATACTGATT GTGAATCTAA TCCATTAGT
   **** ** *** * **
369 : -----ACTG-----CT--GCCACTGTGT

535 : CAGATTTTAG ATGTTAGAGA AGAGTCTTGT GGAACCAGGC CGGACAGTTG CACGGTTGGA
   *** * * **** *
385 : CAG-----G CTCGGT--A

595 : CATCAAGATA TGAATTCTTC GCTGAATTAC GATTGCTGT TAGAGTTTGA GCAGCAGTAT
   * ** * * * **** * *** *****
397 : C-----TGCATTTTCT GATGAAT--- ----CTG--AAGTTTG--

655 : TGGGGCCAAG TTTTGCAGGA GAAAGAGAAA CCGAAGCAGG AAGAAGAGGA GATACAGCAA
   **** * ** *****
425 : -----TGCACGT GA-----G GATACA-----

715 : CAGCAACAGG AACAGCAACA GCAACAGCTG CAACCGGATT TGCTTACTGT TGCAGATTAC
   ** ** *** *** **
441 : -----AA---TG CAA---GAT- ----CT--

775 : GGTGGCCTT GGTCTAATGA TATTGTAAT GATCAGACTT CTTGGGATCC TAATGAGTGC

```

Fig. 4-20

```

                                0010181
****  ** **                    ***** * **      * ***      *
453 : GGT-----TT GG----- --TCAGA--T CT-----C TAA-----C

835 : TTTGATATTA ATGAACCTCT TGGAGATTG AATGAACCTG GTCCCCATCA GAGCCAAGAC
      **          ***      ****
474 : TT----- --CTC-- --GCATTT-----C

895 : CAAAACCACG TAAATTCTGG TAGTTATGAT TTGCATCCGC TTCATCTCGA GCCACACGAT
      *****          **** *  * **  * * ***      *
486 : CAAA----- --TGTTAAG-- -TCCAATAAC TGCAT-----T

955 : GGTCACGAGT TCAATGGTTT GAGTTCTCTG GATATTTGA
      *** * ***      ***  * **      ** * *
513 : GGTTA--AGT ----TGG--G GCGT----- --TACTAG-

```

+++++

```

Sequence 1      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026

```

```

Sequence 2      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 43.40 [%]
Weight           : 252

```

```

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
   *** * **          **      ***
1 : ATGTCATC----- --CA----- --TAG-----

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
     ** * *      * * **  ****      ** * ****
14 : -----AGCC A-----AAA GT--AATG-- -----ATGGTTGGT

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CCAA-AAGGT TCGAGGAAGG GTTGTATGAA
     * * * *  ** ***  ** **  * * ****  ** ***** * *****
37 : GCTAAT-AAG AAACAA--CG AA----CGGT CCAAGCTAGT TCGAGGAAAG GTTGTATGAG

180 : AGGTAAAGGT GGACCTGAAA ACGGGATTG TGAATATAGA GGAGTTAGAC AGAGGAGATG
     *** *****  **** * * * *  * * * *  * * * *  * * * *
90 : AGGAAAAGGT GGACCGGATA ACGCGTCTTG CACTTACAAA GGTGTTAGAC AACGCACTTG

240 : GGGTAAATGG GTTGCTGAGA TCCGTGAGCC AGACGGAGGT GCTAGGTTGT GGCTCGGTAC
     *** *****  ** *****  **** *****  ** * *  * * *****
150 : GGGCAAATGG GTCGCTGAGA TCCGCGAGCC TAACCGAGGA GCTCGTCTTT GGCTCGGTAC

300 : TTTCTCCAGT TCATATGAAG CTGCATTGGC TTATGACGAG GCGG--CCAA AGCTATATAT
     *** **  **  *****  *****  *****  ** * *  * * * *
210 : CTTGACACCC TCCCGTGAAG CTGCCTTGGC TTATGACTCC GCAGCTCGTA AGCTCTATGG

358 : G-GTCAGTCT GCCAGACTCA ATCTTCCCGA GATCACAAT CGCTCTTCTT CGACTGCTGC
     * * ** **  ** *****  * * * *  * * * *  * * *

```

Fig. 4-21

```

270 : GCCTGAGGCT --CA-TCTCA ACCTCCCTGA G-----0010181-----TCCTT AAGAAGTTAC

417 : CACTGCCACT GTGTCAGGCT CGGTTACTGC ATTTTCTGAT GAATCTGAAG TTTGTGCACG
      * ** ** * ** * ** * * **
313 : C-CTAAACG GCGTC-GTCT C-----CGGC -----GTCC---

477 : TGAGGATACA AATGCAAGTT CAGGTTTTGG TCAGGTGAAA CTAGAGGATT GTAGCGATGA
      ** **** * ** * ** * ** * * **
340 : -CAGACTACA ---CCAAG-- CAG---CAAC ACCGGTGGAA --AAAGCA-- GCAGCGA---

537 : ATATGTTCTC TTAGATAGTT CTCAGTGTAT TAAAGAGGAG CTGAAAGGAA AAGAGGAAGT
      *** * ** * * ** * * * * **
384 : -----CTC TGAG-----T CGCCGTG--T TCA-----TCCAACGA- ----GATGT

597 : GAGGGAAGAA CATAACTTGG CTGTTGGTTT TGAATTGGA CAGGACTCGA AAAGGGAGAC
      *** * * * ** * ** * **
416 : -----CATCA-----TG TGGAA-----GAGT-GA CAGAGGAGA-

657 : TTTGGATGCT TGGTTGATGG GAAATGGCAA TGAACAAGAA CCATTGGAGT TTGGTGTGGA
      * **** ** * * ** *
443 : -----TATCATGG GA-----GCATATAAA C-----GTGGA

717 : TGAAACGTTT GATATTAATG AGCTATTGGG TATATTAAC GACAACAATG TGTCTGGTCA
      *** * * ** * ** * **
468 : -----TTT GCCGTAATG -----GATG ATTCT--TCA

777 : AGAGACAATG CAGTATCAAG TGGATAGACA CCCAAATTTC AGTTACCAA CGCAGTTTCC
      * ** *** ** * ** * **
493 : A-----TA-----TGGGAAGAAG CTACAATGTC -GTTA-----GGA-TTTCC

837 : AAATTCTAAC TTGCTCGGGA GCCTCAACCC TATGGAGATT GCTCAACCAG GAGTTGATTA
      ** * ** * ** * ** *
528 : --ATGGGTTC ATG--AAGGA G-----A TAATGATATT TCTC-----GGTTTGATAC

897 : TGGATGTCCT TATGTGCAGC CCAGTGATAT GGAGAACTAT GGTATTGATT TAGACCATCG
      * ** *** * ** *** ** * **
570 : T---TG---TATTT-----CCGGTG-----GCTAT TCTA---ATT GGGA-----

957 : CAGGTTCAAT GATCTTGACA TACAGGACTT GGATTTTGGG GGAGACAAAG ATGTTTCATGG
      *** *** * * **
600 : ----TTC---CTT-TCA TTCCCCACTT -----

1017 : ATCTACATAA
        * *
619 : -----TGA

```

+++++

```

Sequence 1      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026

```

```

Sequence 2      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*NT         : 2

```


Fig. 4-22

0010181

Matching : 47.50 [%]
Weight : 184

```

1 : ATGCCGTCGG -AGATTGTTG ACAGGAAAAG GAAGTCTCGT GGAACACGAG ATGTAGCTGA
   *** ** **** * * * * * ** * * * * * * * * * *
1 : ATGGAAAAGG AAGATAACGG ATCGAAACAG --AG-CTCCT -CTGCTTCTG TTGTATCCTC

60 : GATTCTAAGG CAATGGAGAG AGTACAATGA GCAGATTGAG GCAGAATCTT GTATCGATGG
   ** *** * * * * * * * * * * ** * * * * * * * * * *
57 : GA---GAAGA CGAAGAAGAG TG---GTTGA GCCAGTGGAA GC--GACGTT ACAGAGATG-

120 : TGGTGGTCCA A--AAT---- -CAATCCGAA AGCCTCCTCC AAAAGGTTCTG AGGAAGGGTT
   ** * * * * * * * * * * * * * * * * * * * * * *
108 : -GGAGGAAGA AGGATTGGCG AGAGCTCGTA GGGTTCAAGC CAAAGGTTCTG AAGAAAGGTT

173 : GTATGAAAGG TAAAGGTGGA CCTGAAAACG GGATTTGTGA CTATAGAGGA GTTAGACAGA
   ***** * * * * * * * * * * * * * * * * * * * *
167 : GTATGAGAGG AAAAGGTGGA CCAGAGAATC CTGTTTGTCTG GTTTAGAGGT GTTCGACAAA

233 : GGAGATGGGG TAAATGGGTT GCTGAGATCC GTGAGCCAGA CGGAGGTGCT AGGTTGTGGC
   ** ***** * * * * * * * * * * * * * * * * * *
227 : GGGTTTGGGG GAAATGGGTT GCTGAGATAC GTGAACCAG- -TGAGTCAC- -----C

293 : TCGGTACTTT CTCCAGTTCA TATGAAGCTG CATTGGCTTA TGACGAGGCG GCCAAAGCTA
   *** * * * * * * * * * * * * * * * * * * * * *
275 : GTGGTGCAAA CTCTAG-TCG TAGTAAACGG CTTTGGCTT- -----G GC-----A

353 : TATATGGTCA GTCTGCCAGA CTCAATCTTC CCGAGATCAC AAATCGCTCT TCTTCGACTG
   * * * * * * * * * * * * * * * * * * * * * *
317 : CGTTTGCT-- -ACTG-CAG- CTGAAGCTGC ----- -TTTGGCT-- --TACGACAG

413 : CTGCCACTGC CACTGTGTCA GGCTCGGTTA CTGCATTTTC TGATGAATCT GAAGTTTGTG
   ***** * * * * * * * * * * * * * * * * * *
357 : ----AGCTGC TA--GTGTCA TGTACGG--A C--CCTATGC ----CAGGT TAAATTT--

473 : CACGTGAGGA TACAAATGCA AGTTCAGGTT TTGGTCAGGT GAAACTAGAG GATTGTAGCG
   * * * * * * * * * * * * * * * * * * * * * *
399 : CCCG-GAAGA -----T TTG----GGT G-----GGG GA----AG-G

533 : ATGAATATGT TCTCTTAGAT AGTTCTCAGT GTATTAAAGA GGAGCTGAAA GGAAAAGAGG
   * * * * * * * * * * * * * * * * * * * * * *
424 : AAGAA----- -GGACGA GGAGGCG-- -----GA

593 : AAGTGAGGGA AGAACATAAC TTGGCTGTTG GTTTGGAAAT TGGACAGGAC TCGAAAAGGG
   **** * * * * * * * * * * * * * * * * * *
444 : AAGTTCGGGA ----- --GGCTATTG G--TTGGAA- -----AC T----AACAA

653 : AGACTTTGGA TGCTTGGTTG ATGGGAAATG GCAATGAACA AGAACCATTG GAGTTTGGTG
   * * * * * * * * * * * * * * * * * * * * * *
477 : AGCCGGTAAT GCGTGATTG AAACGGAA-G G---TGGAAA AGA--CTATG TAGTCT----

713 : TGGATGAAAC GTTTGATATT AATGAGCTAT TGGGTATATT AAACGACAAC AATGTGTCTG
   ***** * * * * * * * * * * * * * * * * * *
527 : ACAATGAA-- ----GACGCT ATTGAGC--T TGGCCAT--- ----GACAAG ACTCAGAATC

773 : GTCAAGA--G ACAATGCAGT ATCAAGTGGG TAGACACCCA AATTTCAGTT ACCAAACGCA
   * * * * * * * * * * * * * * * * * *
572 : CT-ATGACTG ATAATGAA-- AT--AGTG-- ----AACCCA GCAGT--GAA ATCAGAGGAA

```

Fig. 4-23

0010181

```

831 : GTTTCCAAAT TCTAACTTGC TCGGAGCCT CAACCCTATG GAGATTGCTC AACCAGGAGT
      * ** *   *** ** ***          ** * ****   *** **
619 : GGTTACA--- GCTA---TGA TCG----- -----ATT CAAATTGGAT AACGGATTGT

891 : TG-ATTATGG ATGTCCTTAT GTGCAGC-CC AGTGATATGG AGAACTATGG TATTGATTAA
      ** ** *   *   *** *   *** ** *** **   ** * **   ** **
659 : TGTATAATGA A---CCTCA- ---AAGCTCC AGT--TAT-- --CACCAGGG AGGTGGATTG

949 : GACCATCGCA GGTTCATGA TCTTGACATA CAGGACTTGG ATTTTGGAGG AGACAAAGAT
      **          **** * * ****          * ****          ****
706 : GA----- --TTCA--TA TTTTGA---- -----GT ATTT----- ----CAGAT

1009 : GTTCATGGAT CTACATAA
        * *   **
731 : -----T C----TAG
  
```

+++++

```

Sequence 1      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026

Sequence 2      : DREB2F.nuc
Size            : 834
Matching Position : 1 - 834
  
```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

Matching         : 48.77 [%]
Weight          : 150
  
```

```

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
   ** ** *   ** **          ** **
1 : AT-----GG AGA----- -----AA--TC--- -----

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
   ** ** *   **** *   ***** ** ****
12 : ATCCT---C AATGAA--- --ACAAT--- -----GG AAGAA-----

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CCAAAAGGTT CGAGGAAGGG TTGTATGAAA
      ***          *** ** *   **
36 : --GGGT--- ----- --CCTGCT C----- --GG-----

181 : GGTAAAGGTG GACCTGAAAA CGGGATTTGT GACTATAGAG GAGTTAGACA GAGGAGATGG
      ***** * ** **** ** ***** * ** * * **** ** ** **** **
49 : GGTAAAGGCG GTCCACAAAA CGCTCTTTGT CAGTACCGTG GAGTCAGGCA AAGGACTTGG

241 : GGTAAATGGG TTGCTGAGAT CCGTGAGCC- -AGACGGAGG TGCTAGGTTG TGGCTCGGTA
      ** ***** * ***** * * ***** *** **** ** ** * ***** **
109 : GGCAAAATGGG TGGCTGAGAT CAGAGAGCCC AAGA-AGAGG -GCAAGACTT TGGCTTGGCT

299 : CTTTCTCCAG TTCATATGAA GCTGCATTGG CTTATGACGA GCGGCCCAAA GCTATATATG
      ***** * *   * * *** ** ** ***** ** *** **   * ****
167 : CTTTCGCTAC AGCTGAAGAA GCAGCTATGG CTTATGATGA GGCTGCCTTG AAACCTCTATG

359 : GTCAGTCTGC CAGACTCAAT CTTCCCGAGA TCACAAATCG CTCTTCTTC- GACTGCTGCC
      * **   **   ***** *** **   ***          ***** * ** * *
227 : GGCACGACGC ATACCTCAA- CTTACC---- TCA----- -TCTTCAGCG GAATAC-AAG
  
```

Fig. 4-24

0010181

```

418 : ACTGCCACTG TGTCAAGGCTC GGTACTGCA TTTTCTGATG AATCTGAAGT TTGTGCACGT
    ** * *** ** * *** * * *** *** * * * * * **
273 : ACCTTCTCTG AGTAACTCTC AG-----A GGTTCAAATG GGT---ACCT TCAAGGAAGT

478 : GAGGATACAA ATG-CAAGTT CAGGTTTTGG TCAGGTGAAA CTAGAGGATT GT-AGCGATG
    *** *** ** ** * *** * * * *** * * * * * ***
323 : --TTATATCT ATGTTTCCTT CA---TGTGG T-ATGCTAAA C--GTGAATG CTCAGCCTAG

536 : AATATGTTCT CTTAGATAGT TCTCAGTGTA TTAAAGAGGA GCTGAAAGGA AAAGAGGAAG
    ***** * *** * *** * * *** ** ** ** ** ** *** **
375 : ----TGTC- ---ACATAAT --CCAGCAAA GACTAGAAGA ACTCAA--GA AAAGTGGACT

596 : TGAGGGAAGA ACATAACTTG GCTGTTGGTT TTGAATTGG ACAGGACTCG AAAAGGGAGA
    * * ** ** ** * *** * * * ** ** ** * *** * *
423 : T---TTATC TCAATCCTAT TCTCTAGTT CT--TCCTCC AC-CGAATCA AAAACTAATA

656 : CTTTGGATGC TTGGTTGATG GGA--AATGG CAATG----A ACA-AGAA-C CATTGGAGTT
    ** ** ** ***** ** * * *** * * *** * ** **
476 : CT----AGC TTTCTTGATG AGAAGACCAG CAAGGGAGAA ACAGACAATA TGTTCGAAGG

708 : TGGTG--TGG ATGAAACGTT TGATATTAAT GAGCTATTGG GTATATTAAC CGACAACAAT
    ***** * * ***** *** * * * * * ** * ** * * ****
531 : TGGTGATCAG AAGAAACCAG AGATCGACCT GACC----GA GTTTCCT--- CAGCAACTAG

766 : GTGTCTGGTC AAGA-GACAA T---GCAGTA TCAAGTGGAT AGACACCCAA ATTTGAGTTA
    * *** * * ** * ** * * ***** * * * * * * * * *
584 : GAATCTTG-A AGGATGAAAA TGAAGCAGAA CCAAGTG--- AGGTAGCAGA GTGTCA-TTC

822 : CCAAACGCAG TTTCCAAATT CTAACCTGCT CGGGAGCCTC AACCCATATG AGATTGCTCA
    ** ***** * *** ** * ** ** * * * * *
639 : CC----- -CTCCACCAT GGAACGAGC- AAGAAG---- AAAGTGAAG TCCTTCAGA

882 : AC-CAGGAGT TGATTATGGA TGTCTTAT- GTGCAGCC-- -CAGTGATAT GGAGAACTAT
    ** ** * * * * * * * * * * * * * * * * * * *
685 : ACTGAGAATT TCAGCTGGGA TACCCTGATC GAGATGCCAA GAAGTGA-AA CCACAACAT

937 : GGTA-TTGA- TTTAG-ACCA TCGCAGGTTT AATGATCTTG A-CATACAGG A--CTTGGAT
    * * **** * * * * * * * * * * * * * * * *
744 : GCAATTTGAC TCCAGCAACT TCGGAAG--C TATGATTTTG AGGATGATGT ATCCTTCCCT

991 : TTTGGAGGAG ACAAAGATGT TCATGGATCT ACATAA
    * * * * * * * * * * * * *
802 : TCCATCTGGG ACTACTACG- -GAAGCTTAG A-TTGA

```

+++++

```

Sequence 1      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

```

Matching : 48.42 [%]

Fig. 4-25

0010181

Weight : 130

```

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
   **          **** * ***          ***
1 : AT----- --GGAA---G AAG----- --AGC---

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
   * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
14 : AACCTCCGGC CA-----AGA ----AACGA- ----- --AA----- --CATGG-

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CCAAAGGTT CGAGGAAGGG TTGTATGAAA
   **          * * * * * * * * * * * * * * * * * * * * * * * * * *
41 : ---GG----- -----AGAT CTAGAAAAGG TTGCATGAAA

181 : GGTAAAGGTG GACCTGAAAA CGGGATTGTG GACTAT-AGA GGAGTTAGAC AGAGGAGATG
   ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
67 : GGTAAAGGCG GTCCAGAGAA CGCCACGTGT -ACTTTCCTG GGAGTTAGGC AACGGACTTG

240 : GGGTAAATGG GTTGCTGAGA TCCGTGAGCC AGACGGAGGT GCTAGGTTGT GGCTCGGTAC
   ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
126 : GGGTAAATGG GTGGCTGAGA TCCGTGAGCC TAACCGTGGG ACTCGTCTCT GGCTCGGCAC

300 : TTTCTCCAGT TCATATGAAG CTGCATTGGC TTATGACGAG GCGGCCAAAG CTATATATGG
   ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
186 : GTTTAATACC TCGGTCGAGG CCGCCATGGC TTACGATGAA GCCGCTAAGA AACTCTATGG

360 : TCAGTCTGCC AGACTCAATC TTCCCGAGAT CACAAATCGC TCTTCTTCGA CTGCTGCCAC
   ** ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
246 : ACACGAGGCT AAACCTCAA-C TTGGTGCACC CACAACAACA ACAACAAGTA GTAGTG-AAC

420 : TGCCACTGTG TCAGGCTC-G GTTACTGCAT TTTCTGATGA ATCTGAAGTT TGTGCACGTG
   * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
304 : AGAAACT-TG TCTTTTCTG GCCACGG--- -GTCGGGT-- -TCTTGGGCT TAT-AATAAG

479 : AGGATACAAA TGCAAGTTCA GGTTTTGGTC AGGTGAAAC- TAGAGGATTG TAGCGATGAA
   * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
355 : AAGCTCGATA TG---GTTCA TGGGTTGGAC CTTGGTCTCG GCCAGGCAAG T--TGTTAC

538 : TATGTTCT-- CTTAGATAGT TCTCAGTGTA TTA----AAG AGGA-GCTGA AAGGAAAAGA
   * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
410 : GAGGTTCTTG CTCAGAGAGA TC-GAGTTT CTACAAGAAG ATGATGATCA TAGTCATAAT

591 : GGAAGTGAG- --GGAAGAAC ATAACTTGGC TGTGTTTGT GGAATTGGAC A---GGAICT
   ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
469 : CGATGTTCTG CTTCAAGTGG TTCGAATCTT TGTGTTTAT -TACCTAAAC AAAGTGATTC

645 : GAAAAG---G GAGACTTTGG ATGCT----- TGGTTGATG- -GGAAATGGC AATGAACAAG
   **          ***** * ***** * * * * * * * * * * * * * * * *
528 : ACAAGATCAA GAGACCGTTA ATGCTACGAC TACTT-ATGG CGGTGAAGGC GGTGGTGGCT

695 : AACCATTGGA GTTT--GGTG TGGATGAAAC GTTTGATATT AATGAG---- --CTATTGGG
   * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
587 : CTACGTTAAC GTTTTCGACC AATTGAAAC CAAAGAATTT GATGAGTCAG AATTATGGAT

747 : TAT---ATTA AACGACAACA ATGTGTCT-- --GGTCAAG- --AGACAATG CAGTATCAAG
   *** ** * * * * * * * * * * * * * * * * * * * * * * * * * * *
647 : TATACAATGG AGCTTGGTCT AGGTTTCTTG TGGGCAAGA AAAGAAGACG GAACATGACG

797 : TG-GATAGAC ACCCAAAT-T TCAGTTACCA AACGCAGTTT CCAAATTCTA ACTTGCTCGG

```

Fig. 4-26

```

                                -0010181
** ** *      ** ** * * ** *      *** *      *** * **** *
707 : TGTCATCGTC GTGTGGATCG TCGGACAACA AGGAGAGTAT GTTGGTTCCT AGTTGCGGCG

855 : GAGCCTCAAC CCTATGGAGA TTGCTCAACC AGGAGTT-GA TTATGGATGT CCTTATGTGC
***          *** ** * * ***** ** * **      *** **
767 : GAG----- ----AGAGG ATGCATAGGC CGGAGTTGGA AGAGCGAACA GGATATTTGG

914 : AGCCCACTGA ---TATGGAG AACTATGGTA TTGATTTAGA CCATCGCAGG TTCAATGATC
*      *** * ***** * ** * * * ***** ** *      *** **
815 : AAATGGATGA TCTTTTGGAG ATTGATGATT TAGGTTT-GT TGATTG---- -GCAAAAATG

971 : TTGACATACA GGACTTGGAT TTTGGAGGAG ACAAAGATGT TCATGGA--T CTACATAA
** * ** ** ***** ** ** *** * * * ***** *      *
869 : GAGA-TTTC AGAATTGGTG TTGTGAAGAG TTTCA-ACAT CCATGGAATT GGTTCGTG

```

+++++

```

Sequence 1      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 48.34 [%]
Weight       : 62

```

```

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
****          ***** ** ***** ***** *****
1 : ATGCC----- ----CAGGAAACGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
***** ***** ***** ***** ** ***** ***** *****
46 : ATTCTAAGGA AATGGAGAGA GTACAATGAG CAGACCGAGG CAGATTCTTG CATCGATGGT

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CAAAAGGTT CGAGGAAGGG TTGTATGAAA
***** ** ** ***** **** ***** ***** ** ***** *****
106 : GGTGGTCCAA AACCAATCCG AAAGCCTCCT CAAAACGTT CGAGGAAGGG TTGTATGAAA

181 : GGTAAGGTG GACCTGAAAA CGGGATTGT GACTATAGAG GAGTTAGACA GAGGAGATGG
***** ***** ***** ***** ** ***** ***** *****
166 : GGTAAGGTG GACCTGAAAA TGGGATTGT GACTATACAG GAGTTAGACA GAGGACATGG

241 : GGTAATGGG TTGCTGAGAT CCGTGAGCCA GACGGAGGTG CTAGGTTGTG GCTCGGTACT
***** ***** ***** * * ***** ** ** ** *****
226 : GGTAATGGG TTGCTGAGAT CCGTGAGCCA GGCCGAGGTG CTAAGTTATG GCTCGGTACT

301 : TTCTCCAGTT CATATGAAGC TGCATTGGCT TATGACGAGG CGGCCAAAGC TATATATGGT
***** ***** ***** ***** ***** * ***** ** **
286 : TTCTCTAGTT CATATGAAGC TGCATTGGCT TATGATGAGG CTTCCAAAGC TATTACGGT

361 : CAGTCTGCCA GACTCAATCT TCCCGAGATC ACAAATCGCT CTTCTTCGAC TGCTGCCACT
***** ***** ***          ** **      **
346 : CAGTCTGCCA GACTCAATCT TCC----- ----AC TG-----CT

```

Fig. 4-27

0010181

```

421 : GCCACTGTGT CAGGCTCGGT TACTGCATT TCTGATGAAT CTGAAGTTTG TGCACGTGAG
*****
375 : GCCACTGTGT CAGGCTCGGT TACTGCATT TCTGATGAAT CTGAAGTTTG TGCACGTGAG

481 : GATACAAATG CAAGTTCAGG TTTTGGTCAG GTGAACTAG AGGATTGTAG CGATGAATAT
*****
435 : GATACAAATG CAAGATCTGG TTTTGGTC-- -----

541 : GTTCTCTTAG ATAGTTCTCA GTGTATTAAG GAGGAGCTGA AAGGAAAAGA GGAAGTGAGG
** ****
463 : -----AGATCTC-----

601 : GAAGAACATA ACTTGGCTGT TGGTTTTGGA ATTGGACAGG ACTCGAAAAG GGAGACTTTG
** ***
470 : -----TA ACT-----

661 : GATGCTTGGT TGATGGGAAA TGGCAATGAA CAAGAACCAT TGGAGTTTGG TGTGGATGAA
475 : -----

721 : ACGTTTGATA TTAATGAGCT ATTGGGTATA TTAAACGACA ACAATGTGTC TGGTCAAGAG
** *
475 : -----TC T-----

781 : ACAATGCAGT ATCAAGTGGA TAGACACCCA AATTCAGTT ACCAAACGCA GTTTCAAAT
****
478 : -----CGCA -TTTCCAA-

841 : TCTAACTTGC TCGGGAGCCT CAACCCTATG GAGATTGCTC AACCAGGAGT TGATTATGGA
490 : -----

901 : TGTCTTATG TGCAGCCCAG TGATATGGAG AACTATGGTA TTGATTAGA CCATCGCAGG
*** * ** *** * **** * * *** **
490 : -----ATG TTAAGTCCA-----AT AACT---GCA TTGGTTAAG-----

961 : TTCAATGATC TTGACATACA GGACTTGGAT TTTGGAGGAG ACAAAGATGT TCATGGATCT
**** ** *
520 : -----TTGG-----GGCGTT

1021 : ACATAA
** **
530 : AC-TAG

```

+++++

Sequence 1 : DREB2D.nuc
Size : 621
Matching Position : 1 - 621

Sequence 2 : DREB2E.nuc
Size : 735
Matching Position : 1 - 735

Matching Condition.

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
*N+          : 2

```

Fig. 4-28

0010181

```

Matching      : 49.93 [%]
Weight        : 81

1 : ATG-----TC ATC--CATAG AG-----CCAAA
   ***          *** * **
1 : ATGGAAAAGG AAGATAACGG ATCGAAACAG AGCTCCTCTG CTTCTGTTGT ATCCTCGAGA

21 : AG-----TAA TGATGGTTG- ----GT----GCTA- ----AT----AAGAA---
    **      **  * * * * *      * *      * *      * *      * *
61 : AGACGAAGAA GAGTGGTTGA GCCAGTGGAA GCGACGTTAC AGAGATGGGA GGAAGAAGGA

48 : -----AC AACGAACCGT CCAAGCTA-- -GTTTCGAGGA AAGGTTGTAT GAGAGGAAAA
    *      * * * * *      * * * * *      * * * * *      * * * * *
121 : TTGGCGAGAG CTCGTAGGT TCAAGCCAAA GGTTCGAAGA AAGGTTGTAT GAGAGGAAAA

97 : GGTGGACCCG ATAACGCGTC TTGCACTTAC AAAGGTGTTA GACAACGCAC TTGGGGCAAA
    * * * * *      * * * * *      * * * * *      * * * * *      * * * * *
181 : GGTGGACCAG AGAATCCTGT TTGTCGGTTT AGAGGTGTTT GACAAAGGGT TTGGGGGAAA

157 : TGGGTCGCTG AGATCCGCGA GCC-----T AACCGAGGAG C-----TCGT-----
    * * * * *      * * * * *      * * * * *      * * * * *      * * * * *
241 : TGGGTTGCTG AGATACGTGA ACCAGTGAGT CACCGTGGTG CAAACTCTAG TCGTAGTAAA

196 : ---CTTTGGC TCGGTACCTT CGACACCTCC CGTGAAGCTG CTTTGGCTTA TGACTCCGCA
    * * * * *      * * * * *      * * * * *      * * * * *      * * * * *
301 : CGGCTTTGGC TTGGCAGGTT TGCTACTGCA GCTGAAGCTG CTTTGGCTTA CGACAGAGCT

253 : GCTCGTAAGC TCTATGGGCC TGAGGCTCAT CTCAACCTCC CTGAGTCCTT AAGAAGTTAC
    * * * * *      * * * * *      * * * * *      * * * * *      * * * * *
361 : GCTAGTGCA TGTACGGACC CTATGCCAGG TTAAATTTC CGGAAGATT GGTGGGGGA

313 : CCTAAAACGG CGTCGTCTCC GCGTCCAG ACTACACCAA GCAGCAACAC CGGTGGAAAA
    * * * * *      * * * * *      * * * * *      * * * * *      * * * * *
421 : AGGAAGAAG- -GACG----A GGAGGCGGAA AGTTCGGGAG GC-----TAT TGTTG-GAA

373 : AGCAGCAGCG ACTCTGAGTC GCCGTG-TTC ATCC--AACG -AGATGTCAT CATGTGG--A
    * * * * *      * * * * *      * * * * *      * * * * *      * * * * *
469 : ACTAACAAG CCGGTAA--T GCGGTGATTG AAACGGAAGG TGGAAAAGAC TATGTAGTCT

427 : AGAGTGACAG AGGAGAT--A TCATGGGAGC AT-ATAA-AC GTGA----T TTG-CCGGTA
    * * * * *      * * * * *      * * * * *      * * * * *      * * * * *
527 : ACAATGA-AG ACGCTATTGA GCTTGG--CC ATGACAAGAC TCAGATCCT ATGACTGATA

478 : ATGGA----T G-ATTCTTCA ---ATATGGG AAGAA-GCTA CAATGTCGTT AGGATTTCCT
    * * * * *      * * * * *      * * * * *      * * * * *      * * * * *
584 : ATGAAATAGT GAACCCAGCA GTGAAATCAG AGGAAGGTTA CAGCTATGAT -CGATTCAAA

529 : TGGGTTTCATG AA--GGAG-A TAATGATATT TCTCGGTTTG ATACTTGTAT TTCCGGTGG-
    * * * * *      * * * * *      * * * * *      * * * * *      * * * * *
643 : TTGGATAACG GATTGTTGTA TAATGA-ACC TCAAAGCT-- CCAGTTATCA CCAGGGAGGT

585 : CTATTCTAAT TGGGATTCCT TTCATTCCCC ACTTTGA
    * * * * *      * * * * *      * * * * *      * * * * *
700 : GGATTC-GAT TCATATTTTG AGTATTTTCA ATTCTAG

```

+++++

Sequence 1 : DREB2D.nuc
 Size : 621
 Matching Position : 1 - 621

Fig. 4-29

0010181

Sequence 2 : DREB2F.nuc
Size : 834
Matching Position : 1 - 834

Matching Condition.

Matches : -1
Mismatch : 1
Gaps : 1
*N+ : 2

Matching : 46.13 [%]
Weight : 164

```

1 : ATGTCATCCA TAGAGCCAAA AGTAATGATG GTTGGTGCTA ATAAGAAACA ACGAACCGTC
   ***          *** ** *          * * ** * * * * * * *
1 : ATG----- --GAG--AA A----- --TCATCCTC A-ATGAAACA A-----

61 : CAAGCTAGTT CGAGGAAAGG TTGTATGAGA GGAAAAGGTG GACCCGATAA CGCGTCTTGC
   * ** ** * * * * * * * * * * * * * * * * * * * *
28 : -----T GGAAGAAGGG TCCTGCTCGG GGTAAGGCG GTCCACAAAA CGCTCTTTGT

121 : ACTTACAAAG GTGTTAGACA ACGCACTTGG GGCAAATGGG TCGCTGAGAT CCGCGAGCCT
   *** * * * * * * * * * * * * * * * * * * * * *
79 : CAGTACCGTG GAGTCAGGCA AAGGACTTGG GGCAAATGGG TGGCTGAGAT CAGAGAGCCC

181 : AA-CCGAGGA GCTCGTCTTT GGCTCGGTAC CTTCGACACC TCCCGTGAAG CTGCCTTGGC
   ** **** ** * **** **** ** * **** ** * **** ** *
139 : AAGAAGAGG- GCAAGACTTT GGCTTGGCTC TTTCGCTACA GCTGAAGAAG CAGCTATGGC

240 : TTATGACTCC GCAGCTCGTA AGCTCTATGG GCCTGAGG-- ----- ---CTCATCT
   ***** ** ** * * ***** ** ** * *****
198 : TTATGATGAG GCTGCCTTGA AACTCTATGG GCACGACGCA TACCTCAACT TACCTCATCT

285 : ----- -CAA---CCT CCCTGAGT-- CCTTAAGAAG T----- TACCCTAAA-
   *** * * * ***** * * *** * * *****
258 : TCAGCGGAAT ACAAGACCTT CTCTGAGTAA CTCTCAGAGG TTCAAATGGG TACCTTCAAG

319 : -----ACG GCGTCGTCTC C-----GG -----C GT-----CCC AGACT-----
   * * * * * * * * * * * * * * * * * * * *
318 : GAAGTTTATA TCTATGTTTC CTTTATGTGG TATGCTAAAC GTGAATGCTC AGCCTAGTGT

346 : --ACACCAAG CAGC-AACAC CGGTGGAA-- ----AAAGC- -----
   *** * **** * * * * * * * * * * * *
378 : TCACATAATC CAGCAAAGAC TAGAAGAACT CAAGAAAACCT GGACTTTTAT CTCAATCCTA

376 : -----AG- -----CA GCG----- -ACTCTGAGT CGCCGTGTTT AT-----C
   ** ** ** * * * * * * * * * * * *
438 : TTCTTCTAGT TCTTCTCCA CCGAATCAAA AACTAATACT AGCTTTCTTG ATGAGAAGAC

405 : CAAC----GA GA---TGTC TCATG-TGGA AG--AGTGA- CAGAGG---- -AGATAT---
   ** * ** ** * * * * * * * * * * * *
498 : CAGCAAGGGA GAAACAGACA ATATGTTTCA AGTGTTGAT CAGAAGAAAC CAGAGATCGA

446 : CATG----- --GGAGC A--TA----- --TAAACG-T GGATTG--- ----CC---
   * ** ** * * * * * * * * * * * *
558 : CCGTACCGAG TTTCTTCAGC AACTAGGAAT CTTGAAGGAT GAAAATGAAG CAGAACCAAG

474 : ---GGTAATG GA---TGATT ---CTTCAAT ATGG----- ---GAAGAAG CTACAATGTC
   **** ** * *** ** ** * * * * * *
618 : TGAGGTAGCA GAGTGTCAAT CCCCTCCACC ATGGAACGAG CAAGAAGAAA CTGGAA-GTC

```


Fig. 4-30

0010181

```

516 : GTT----- --AGGATTC -CATGGGT- -CATGAAGGA GAT----- AATGA-----
      **          ** *****      * * * * *      * * * * *      * * *
677 : CTTTCAGAAC TGAGAATTC AGCTGGGATA CCCTGATCGA GATGCCAAGA AGTGAAACCA

552 : -TATTTCTCG GTTTGATACT TGTATTTCCG GTGGCTATTC TAATTGGGAT -----TCCT
      * * *      ***** * * * * * * * * * * * * * * * * * * * * *
737 : CAACTATGCA ATTTGACTCC AGCAACTTCG GAAGCTATGA TTTTGAGGAT GATGTATCCT

605 : TTCATTCC-- -----CCAC T----- --TTGA
      * * * * *      * * * * *      * * * * *
797 : TCCCTTCCAT CTGGGACTAC TACGGAAGCT TAGATTGA

```

+++++

```

Sequence 1      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 45.04 [%]
Weight            : 190

```

```

1 : ATGTCATCCA TAGAGCCAAA AGTAATGATG GTTGGTGCTA ATAAGAAACA ACGAACCGTC
   ***          ** ** ** * * * * *      * * * * *      * * * * *
1 : ATG----- --GA-AGAAG AGCAA----- ---CCTCCGG CCAAGA---A ACGAAACAT-

61 : CAAGCTAGTT CGAGGAAAGG TTGTATGAGA GGAAAAGGTG GACCCGATAA CGCGTCTTGC
     * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
39 : --GGGGAGAT CTAGAAAAGG TTGCATGAAA GGTAAAGGCG GTCCAGAGAA CGCCACGTGT

121 : ACTTACAAAG GTGTTAGACA ACGCACTTGG GGCAAATGGG TCGCTGAGAT CCGCGAGCCT
     **** * * * * * * * * * * * * * * * * * * * * * * * * * * *
97 : ACTTTCCGTG GAGTTAGGCA ACGGACTTGG GGTAAATGGG TGGCTGAGAT CCGTGAGCCT

181 : AACCGAGGAG CTCGTCTTTG GCTCGGTACC TTCGACACCT CCCGTGAAGC TGCCTTGGCT
     ***** ** * * * * * * * * * * * * * * * * * * * * * * *
157 : AACCGTGGGA CTCGTCTCTG GCTCGGCACG TTAATACCT CGGTCGAGGC CGCCATGGCT

241 : TATGACTCCG CAGCTCGTAA GCTCTATGGG CCTGAGGCTC ATCTCAAC-- ----CTCCCT
     ** ** * * * * * * * * * * * * * * * * * * * * * * *
217 : TACGATGAAG CCGCTAAGAA ACTCTATGGA CACGAGGCTA AACTCAACTT GGTGCACCCA

295 : GA-----GTC CTTAAGAAGT --TACCCTAA AAC----- --GGC-- --GTCG--
     * * * * * * * * * * * * * * * * * * * * * * *
277 : CAACAACAAC AACAAGTAGT AGTGAACAGA AACTTGTCTT TTTCTGGCCA CGGGTCGGGT

328 : TCTCCGGC-- -----G TC----CCAG
     *** ***      * * * * *
337 : TCTTGGGCTT ATAATAAGAA GCTCGATATG GTTCATGGGT TGGACCTTGG TCTCGGCCAG

343 : AC-----TA CACCAAG--- -----CAGCA ACACCG---G TGGAAAAAGC AGCAGCGACT

```

Fig. 4-31

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      *   *   *** *   ***   * * *   *   *   *   *
397 : GCAAGTTGTT CACGAGGTTT TGGCTCAGAG AGATCGAGTT TTCTACAAGA AGATGATGAT

      *   *   *   *   *   *   *   *   *   *   *   *
386 : CTGAGTC--- -GCCGTGTTT ATC---CAA--- ---CGA--- ---GAT-GTC ATCATGTGGA
      *   ****   *   ****   **   ***   ***   *   *   *   *   *
457 : CATAGTCATA ATCGATGTTT GTCTTCAAGT GGTTCGAATC TTTGTTGGTT ATTACCTAAA

      *   *   *   *   *   *   *   *   *   *   *   *
427 : -AGAGTGA-- CAGAGGA--- ----- -GA -TA-TCATGG ---GA---
      *   ****   **   *   *   *   *   *   *   *   *   *
517 : CAAAGTGATT CACAAGATCA AGAGACCGTT AATGCTACGA CTAGTTATGG CGGTGAAGGC

      *   *   *   *   *   *   *   *   *   *   *   *
453 : -----GC- --ATATAAAC GT----- ----- -GGATTT GCCG-GT---
      **   *   *   *   *   *   *   *   *   *   *   *
577 : GGTGGTGGCT CTACGTTAAC GTTTTCGACC AATTGAAAC CAAAGAATTT GATGAGTCAG

      *   *   *   *   *   *   *   *   *   *   *   *
477 : ----- -AATGG ----- ATGATTCTT- ----CAATA TGGGAAGAAG
      ****   *   *   *   *   *   *   *   *   *   *   *
637 : AATTATGGAT TATACAATGG AGCTTGGTCT AGGTTTCTTG TGGGGCAAGA AAAGAAGACG

      *   *   *   *   *   *   *   *   *   *   *   *
506 : CTACA----- -AT-GTC GTTAGGAT-- ----- -TTCC-
      ***   **   ***   *   ****   ****   *   *   *   *
697 : GAACATGACG TGTCATCGTC GTGTGGATCG TCGGACAACA AGGAGAGTAT GTTGGTTCTT

      *   *   *   *   *   *   *   *   *   *   *   *
528 : ----- -ATGGGT TCAT----- -GAAG ---GA---G ATA-----
      **   *   ***   ****   ****   **   *   *   *
757 : AGTTGCGGCG GAGAGAGGAT GCATAGGCCG GAGTTGGAAG AGCGAACAGG ATATTTGGAA

      *   *   *   *   *   *   *   *   *   *   *   *
548 : ----ATGATA TTTCTCGGTT TGAT-ACTT- -GTATTTCCG GTGGCTA--- -----TTC
      *****   ***   *   *   *   *   *   *   *   *   *   *
817 : ATGGATGATC TTTTGGAGAT TGATGATTTA GGTGTTGTTGA TTGGCAAAAA TGGAGATTTC

      *   *   *   *   *   *   *   *   *   *   *   *
591 : --TAATTGG- ----GATTC CTTTCATTCC CCA----- --CTTTGA
      *****   **   ****   ***   ****   *   *   *
877 : AAGAATTGGT GTTGTGAAGA GTTCAACAT CCATGGAATT GGTCTGA

```

+++++

```

Sequence 1      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 47.49 [%]
Weight            : 113

```

```

1 : ATG----- -TCAT----- CCA----TAG ----- -AGCCA----
   ***          ** *          * *   ***          ** *
1 : ATGCCCAGGA AACGGAAGTC TCGTGAACA CGAGATGTAG CTGAGATTCT AAGGAAATGG

19 : --AAAGT--A ATG----- -ATGG TTGGTGCT-A ATAAGAAACA
    * *** * ***          ** *   ***** *   * * * *
61 : AGAGAGTACA ATGAGCAGAC CGAGGCAGAT TCTTGCATCG ATGGTGGTGG TTCAAACCA

```

Fig. 4-32

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```

51 : A--CGAA--- -CCGTCCAAG CTAGTTCGAG GAAAGGTTGT ATGAGAGGAA AAGGTGGACC
* **** * ***** ***** *** ***** **** * *****
121 : ATCCGAAAGG CTCCTCCAA- AACGTTTCGAG GAAGGTTGT ATGAAAGGTA AAGGTGGACC

105 : CGATAACGCG TCTTGCACTT ACAAAGGTGT TAGACAACGC ACTTGGGGCA AATGGGTCCG
** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
180 : TGAAATGGG ATTTGTGACT ATACAGGAGT TAGACAGAGG ACATGGGGTA AATGGGTTCG

165 : TGAGATCCGC GAGCCTAACC GAGGAGCTCG TCTTTGGCTC GGTACCTTCG ACACCTCCCG
***** ***** ** **** * * * * * * * * * * * * * * * *
240 : TGAGATCCGT GAGCCAGGCC GAGGTGCTAA GTTATGGCTC GGTACTTCT CTAGTTCATA

225 : TGAAGCTGCC TTGGCTTATG ACTCCGCAGC TCGTAAGCTC TATGGGCCTG AGGCTCATCT
***** ***** * * * * * * * * * * * * * * * *
300 : TGAAGCTGCA TTGGCTTATG A----- ------ ------TG AGGCT--TC-

285 : CAACCTCCCT GAGTCCTTAA GAAGTTACCC TAAAACGGCG TCGTCTCCGG CGTCCCAGAC
*** ** * * * * * * * * * * * * * * * * * * * *
330 : CAA----- -AG--CT--- --ATT----- -ACGG-- -----TCAGT C-TGCCCCGAC

345 : TACACCAAGC AGCAACACCG GTGGAAAAAG CAGCAGCGAC TCTGAGTCGC CGTGTTCATC
* * * * * * * * * * * * * * * * * * * * * *
359 : T----CAATC TTC--CA--- ------ CTGCTGCCAC TGTGTCAGGC TCGGTT----

405 : CAACGAGATG TCATCATGTG GAAGAGTGAC AGAGGAGATA TCATGGGAGC ATATAAACGT
** ** * * * * * * * * * * * * * * * * * * * *
396 : --AC-----TG -CATTTTCT- GATGAAT--C TGAAGTTGT GCACGTGAGG ATACAAA---

465 : GGATTGGCCG GTAATGGATG ATTCTTCAAT ATGGGAAGAA GCTACAATGT CGTTAGGATT
*** * * * * * * * * * * * * * * * * * * * * *
443 : -----TGCAA GATCTGGTT- -TTGGTCA-- ------GA TCTCTAACT C--TCGCATT

525 : TCCATGGGTT CATGAAGGAG ATAATGATAT TTCTCGGTTT GATACTTGTA TTTCCGGTGG
*** * * * * * * * * * * * * * * * * * * * * *
484 : TCC----- ------ AAAATGTTA- ------AGTCC AATAACTGCA T-----TGG

585 : CTATTCTAAT TGGGATTCCT TTCATTCCCC ACTTTGA
** * * * * * * * * * * * * * * * *
515 : TTA-----AGT TGGG----- -GCGTT----- AC--TAG

```

+++++

```

Sequence 1      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

```

Sequence 2      : DREB2F.nuc
Size            : 834
Matching Position : 1 - 834

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 48.77 [%]
Weight       : 145

```

Fig. 4-33

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```

1 : ATGGA-AAAG GAAGAT-AAC GGATC---GA AACAGAGCTC CTCTGCTTCT GTTGATATCC-
***** ** * ** * * * * * * * * * * * * * *
1 : ATGGAGAAAT CATCCTCAAT GAAACAATGG AAGAAGGGTC --CTGCTCGG GGTAAGGGCG

55 : -TCGAGAAGA CG----- AAGAAGAGTG G-TTGAGCCA GTGGA----- AGCGA---CG
** * ** * ** * * * * * * * * * * * * * *
59 : GTCCACAAAA CGCTCTTTGT CAGTACCGTG GAGTCAGGCA AAGGACTTGG GGCAAATGGG

97 : TTACAGAGAT --GGGAG--G AAGAAGGATT GGCGAGAGCT CG--TAGGGT -TCAAGCCAA
* * ***** * ** * * * * * * * * * * * * *
119 : TGGCTGAGAT CAGAGAGCCC AAGAAG--AG GGCAAGACTT TGGCTTGGCT CTTTCGCTAC

150 : AGGTTCAAG AA--AGGT-T G---TATGA- GAG----- -GAAA----A GGTG---GAC
** * **** ** * * * * * * * * * * * * * *
177 : AGCT--GAAG AAGCAGCTAT GGCTTATGAT GAGGCTGCCT TGAAACTCTA TGGGCACGAC

188 : -CAGA---GA A-----TCC TGTTTGTCGG TTTAGAGG-- --TGTTGAC AAAGGGTTTG
** * * * * * * * * * * * * * * * * * *
235 : GCATACCTCA ACTTACCTCA TCTTCAGCGG AATACAAGAC CTCTCTGAG TAACCTCAG

234 : GGG--GAAAT GGGTTGC-TG AGATACGTGA ACCAGTGAGT CACCGTGGTG -CAAACTCTA
** ***** ** * * * * * * * * * * * * *
295 : AGGTTCAAAT GGGTACCTTC AAGGAAGTTT ATATCTATGT TTCCTTCATG TGGTATGCTA

290 : GTCGT-AGTA AACGGCTTTG GCTTGGCAGC TT--TGC--- TACT-GCAG- -CTGAAG---
*** * * * * * * * * * * * * * * * * *
355 : AACGTGAATG CTCAGCCTAG TGTTACATA ATCCAGCAAA GACTAGAAGA ACTCAAGAAA

338 : -CTG---CTT TGGCTTACGA CAGAGCTGCT AGTGTATGT ACGGACCCTA TGCCAGGTTA
*** ** * * * * * * * * * * * * * * * *
415 : ACTGGACTTT TATCTCAATC CTATTCTTCT AGT-TCTTCC TC-CACCGAA TCAAAAACCTA

394 : AATTTCCCGG AAGATTTGGG TGGGGGA--A GGAAGAAGGA CGAGGAGGCG GAAAGTTCCG
* * * * * * * * * * * * * * * * * *
473 : A---TACTAG CTTTCTTGAT GAGAAGACCA GCAAG--GGA GAAACAGACA ATATGTTCC--

452 : GAGGCTATTG GTTGGAAGCT AACAAAGCCG GTAATG-GCG TGATTGAAAC GGAAGGTGGA
** * * * * * * * * * * * * * * * *
526 : GAAGGTGGTG ATCAGAAGAA ACCAGAGATC GACCTGACCG AGTTTCTTCA GCAACTAGGA

511 : AAAGACTATG TAGTCT-ACA ATGA---AGA CGCTATTGAG CTTGGCCA-T GACAAGACTC
* * * * * * * * * * * * * * * * *
586 : A---TCT-TG AAGGATGAAA ATGAAGCAGA ACCAAGTGAG GTAGCAGAGT GTCATTCCCC

566 : AGAATCCTAT GACTGATAAT GAA-ATAGT- GAA--CC--- CAGCAGTGA- AATCAGAGGA
* ** ** * * * * * * * * * * * *
642 : TCCA-CCATG GAACGAGCAA GAAGAACTG GAAGTCCTTT CAGAAGTGAAG AATTCAGCT

618 : AGGTTACAGC TATGATC--G ATTCAAATTG GATAACGGAT TGTGTATAA TGAACCTCAA
** * * * * * * * * * * * * * * *
701 : GGGATA---C CCTGATCGAG ATGCCAAGAA GTGAAACCAC AACTATGCAA TTTGACTCCA

676 : --AGCTCC-- -AGTTATCA- --CCAGGGAG GTGGA---TT CGATTATAT TTTGAGTATT
* * * * * * * * * * * * * * *
758 : GCAACTTCGG AAGCTATGAT TTTGAGGATG ATGTATCCTT CCCTTCCATC TGGGACTACT

725 : TCAGATTC-T AG-----
* * * * *
818 : ACGGAAGCTT AGATTGA

```

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60/94

Fig. 4-35

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```

525 : CTACAATGAA G---ACGCTA ---TTGAGCT TGGCCATGAC AAGA-----
      ***** * *      ***      ** * * * * * * * *
648 : ATACAATGGA GCTTGGTCTA GGTTCCTTGT GGGGCAAGAA AAGAAGACGG AACATGACGT

563 : CTCA----- ---GAATCCT ATGACTGATA ATGA-AATA- GT--GAACCC AG-----
      ***      * * * * *      *** * * * * * * * * * *
708 : GTCATCGTCG TGTGGATCGT CGGAC-AACA AGGAGAGTAT GTTGGTTCCT AGTTGCGGCG

602 : --CAGTGAAA TCAGAGGAAG --GTT---AC AGC---TATG ATCGATTCAA A-----
      * * * * * * * * * *      *** * * * * * * * * *
767 : GAGAGAGGAT GCATAGGCCG GAGTTGGAAG AGCGAACAGG ATATTGGAA ATGGATGATC

643 : --TTGGATAA CG--GATTGT TGTATAATGA ACCTCAAAGC TCCAGTTATC ACCA--GGGA
      ***** * * * * *      ** * * * *      ***** * * * * * * *
827 : TTTTGGAGAT TGATGATTTA GGTTCGTTGA TTGGCAAAAA TGGAGATTTC AAGAATTGGT

697 : GGTG-GATTC GATTCATATT TTGAGTATTT CAGATTCTAG
      * * * * * * * * * *      * * * * * * * * *
887 : GTTGTAAGA GTTCAACAT CCATGGAATT --GGTCTGA

```

+++++

```

Sequence 1      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 48.72 [%]
Weight            : 93

```

```

1 : AT-----GGA AAAGGAAGAT AACGGATCGA A-AC-AGA-G CTCCTCTGCT TCTGTTGTAT
  **      *** ** * * * * *      ** * * * * * * * * * *
1 : ATGCCCAGGA AACGGAAG-T CTCG--TGA ACACGAGATG TAGCTGAGAT TCTAAGGAA-

53 : CCTCGAGAAG ACGAAGAAGA GTGTTGAGC CAGTGGAAGC GACGTACAG AGATGGGAGG
  * * * * * * * * * *      ** * * * * * * * * *
57 : -ATGGAG-AG AGTACAATGA G-----CAGA CCGAGGCAGA TTC-TTGCAT CGATGG----

113 : AAGAAGGATT GCGAGAGCT CGTAGGGTTC AAGCCAAAGG TTCGAAGAAA GGTTGTATGA
  * * * * *      * * * * * * * * * *      * * * * * * * * *
105 : -TGGTGGTTC AAAACCAATC CGAAAGGCTC CTCCAAACG TTCGAGGAAG GGTTGTATGA

173 : GAGGAAAAGG TGGACCAGAG AATCCTGTTT GTCGGTTTAC AGGTGTTTCA CAAAGGGTTT
  *** * * * * * * * * * *      *** * * * * * * * * * *
164 : AAGGTAAAGG TGGACCTGAA AATGGGATTT GTGACTATAC AGGAGTTAGA CAGAGGACAT

233 : GGGGGAAATG GGTGCTGAG ATACGTGAAC CAGTGAGTCA CCGTGGTGCA AACTCTAGTC
  **** * * * * * * * * * *      ** * * * * * * * * *
224 : GGGGTAAATG GGTGCTGAG ATCCGTGAGC CAG-----G CCGAGGTGC- -----

293 : GTAGTAAACG GCTTTGGCTT GGCACGTTTG CTAAGCTGCT TGAAGCTGCT TTGGCTTACG

```

Fig. 4-36

```

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***  * * ***** ** ** ** *** * ** ***** *
267 : ----TAA--- GTTATGGCTC GGTACTTTCT CTAGTTCATA TGAAGCTGCA TTGGCTTATG

353 : ACAGAGCTGC TAGTGTCATG TACGGACCCT ATGCCAGGTT AAATTTCCCG GAAGATTTGG
*   *** * * * ** ***** * * **** * * *** * **
320 : ATGAGGCTTC CAAAGCTATT TACGGTCAGT CTGCCCGACT CAATCTTCC- -----

413 : GTGGGGGAAG GAAGAAGGAC GAGGAGGCGG AAAGTTCGGG AGGCTATTGG TTGGAAACTA
**          **          * * * * * **** * ** ** ***
369 : -----AC -----TGCTG CCACTGTGTC AGGC--TCGG TT----ACT-

473 : ACAAAGCCGG TAATGGCGTG ATTGAAACGG AAGGTGGAAG AGACTATGTA GTCTACAATG
**          **          * * ***** * * **          * ***
399 : ----GC--- --ATTTCTG A-TGAATCTG AAG----- --TTGT- -----

533 : AAGACGCTAT TGAGCTTGGC CATGACAAGA CTCAGAATCC TATGACTGAT AATGAAATAG
**          ****          ****          ****          *** * ****
426 : ----GCACG TGAG----- -----GAT A--CAAAT--

593 : TGAACCCAGC AGTGAATCA GAGGAAGGTT ACAGCTATGA TCGATTCAAA TTGGATAACG
** * * * ****          ****          * * ** ** ** ** * * **
444 : -----GC A---AGATC- -----TGTT -TTGGTCAGA TC---TCTAA CT---TCTCG

653 : GATTGTTGTA TAATGAACCT CAAAGCTCCA GTTATCACCA GGGAGGTGGA TTCGATTCAT
** ** * **** * ** ***** ** **          ** * ** *
480 : CAT--TTCCA AAATG----T TAA--GTCCA ---ATAAC-- -----TGCA TTGG-----

713 : ATTTTGAGTA TTTCAGATTC TAG
** ***          * * * ***
515 : ---TTAAGTT GGGGCGTTAC TAG

```

+++++

```

Sequence 1      : DREB2F.nuc
Size            : 834
Matching Position : 1 - 834

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 54.15 [%]
Weight       : 19

```

```

1 : ATGG-AGAA- ATCATCCTC- -----AA TGAACAATG GAAG----- -AAGGGTCTT
**** ***** * ** **** ** ***** * * ** ** ***** *
1 : ATGGAAGAAG AGCAACCTCC GGCCAAGAAA CGAAACATGG GGAGATCTAG AAAAGGT--T

43 : GCTCG--GGG TAAAGGCGGT CCACAAAACG CTCTTTGTCA GTACCGTGGA GTCAGGCAAA
** * ** ***** ***** * * ** * ***** ** *****
59 : GCATGAAAGG TAAAGGCGGT CCAGAGAACG CCACGTGTAC TTTCCGTGGA GTTAGGCAAC

101 : GGAAGTTGGG CAAATGGGTG GCTGAGATCA GAGAGCCCAA GAAGAGGGCA AGACTTTGGC
***** ***** ***** * ***** ** ** * * ** *****

```

Fig. 4-37

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```

119 : GGA CT TGGGG TAAATGGGTG GCTGAGATCC GTGAGCCTAA CCGTGGGACT CGTCTCTGGC

161 : TTGGCTCTTT CGCTACAGCT GAAGAAGCAG CTATGGCTTA TGATGAGGCT GCCTTGAAAC
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
179 : TCGGCACGTT TAATACCTCG GTCGAGGCCG CCATGGCTTA CGATGAAGCC GCTAAGAAAC

221 : TCTATGGGCA CGACGCATAC CTCAACTT-- -----ACC TCATCTTCAG C-----
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
239 : TCTATGGACA CGAGGCTAAA CTCAACTTGG TGCACCCACA ACAACAACAA CAAGTAGTAG

263 : GGAATACAA- ---GACCTTC TCTGAGTAAC ---TC----T C-AGAGGTTT AAATGGGTAC
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
299 : TGAACAGAAA CTTGTCTTTT TCTG-GCCAC GGGTCGGGTT CTTGGGCTTA TAATAAGAAG

311 : CTTCAAGGAA GTTTAT---- ---ATCTATG TTTCTTCAT G--TGGTATG CTAAACGTGA
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
358 : C-TCGATATG GTTCATGGGT TGGACCTTGG TCTCGGCCAG GCAAGTTGTT CACGAGGTTC

362 : ATGCTCAGCC TAGTGTTCAC ATAATCCAGC AAAGACTAGA AGAACTCAAG AAAACTGGAC
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
417 : TTGCTCAG-- -AGAGATCGA GTTTTCTA-C AAGAAGATGA TGATCATAGT CATAATCGAT

422 : TTTTATC-TC AA----TCCT ATTCTT--CT AGTTCTT-CC TCCACCGAAT CAAAACTAA
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
473 : GTTCGTCTTC AAGTGGTTTC AATCTTTGTT GGTATTACC TAAACAAAGT GATTACAAG

474 : TACTAGCTTT C-TTGATGAG AAGACCAGCA AGGGAGAAAC AGACAAT--- --ATGTTTCG-
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
533 : ATCAAGAGAC CGTTAATGCT ACGACTAGTT ATGGCGGTGA AGGCGGTGGT GGCTCTACGT

527 : -AAGGTGGT- GATC-AGAAG AAACCAGAGA --TCGACCTG ACCGAGTTTC TTCAGCA-AC
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
593 : TAACGTTTTT GACCAATTTG AAACCAAGA AATTGATGAG TCAGA-ATTA TGGATTATAC

581 : TAGGAATCTT G---AAGGAT GAAAATGAAG CAGAACCAAG TGAGGTAGCA -GA-GTGTC
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
652 : AATGGAGCTT GGTCTAGGTT TCTTGTGGGG CAAGAAAAGA AGACGGAACA TGACGTGTCA

636 : T--TCCCTC CACCATGGAA CGAGCAAGAA GAAACTGGAA GTCCTTTCAG AACTGAGAAT
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
712 : TCGTCGTGTG GATCGTCGGA C-AACAAGGA GA----GTAT GTTGGTTC-- --CT---AGT

694 : TTCAGCTGGG ATACCTGAT CGAGATGCCA AGAAGTGAAA CCACAATAT GCAATTTG--
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
760 : TCGCGCGGAG AGA---GGAT GCATAGGCC- GGAGTTGGAA GAGCGAACAG GATATTTGGA

752 : ACTCCAGCAA CTTCCGGAAGC T--ATGATT- -----TTG A--GG--ATG ATGTATCCTT
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
816 : AATGGATGAT CTTTGGAGA TTGATGATT AGGTTTGTG ATTGGCAAAA ATGGAGATT

798 : C---CCTTCC ATCTGGG--- -----ACT ACTACGGAAG CTTAGAT-TG A
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
876 : CAAGAATTGG TGTGTGAAG AGTTTCAACA TCCATGGAA- -TTGGTCTG A
  
```

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```

Sequence 1      : DREB2F.nuc
Size            : 834
Matching Position : 1 - 834
  
```

```

Sequence 2      : DREB2H.nuc
  
```


Fig. 4-38

0010181

Size : 534
 Matching Position : 1 - 534

Matching Condition.

Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2

 Matching : 41.63 [%]
 Weight : 254

```

1 : ATGGAGAAAT CATCCTCAAT GAAACAATGG AAGAAGGGTC CTGCTCGGGG TAAAGGCGGT
   ***          * * ***** ** ***          **** **   **
1 : ATG----- ---CCCAG GAAAC---GG AAG----- --TCTCGTGG --AA-----

61 : CCACAAAACG CTCTTTGTCA GTACCGTGGG GTCAGGCAAA GGAAGTGGGG CAAATGGGTG
   *** * *      ***          * ** * * * ** **          *****
29 : -CACGAGA-- ---TGT-- ---AGCTGA G--ATTCTAA GG----- -AAATGG--

121 : GCTGAGATCA GAGAGCCCAA GAAGAGGGCA AGACTTTGGC TTGGCTCTTT CGCTACAGCT
      * ***** ** * ***      ****   ** * ****
61 : -----A GAGAGTACA- -ATGAG---C AGACCGAGGC -AGATTCTT- -----

181 : GAAGAAGCAG CTATGGCTTA TGATGAGGCT GCCTTGAAAC TCTATGGGCA CGACGCATAC
      *** * ****   ** **          ** *** * ** * * * * *
95 : -----GCAT CGATGG---- TGGTG----- --GTTCAAAA CCAATCCGAA AGGCTCCT-C

241 : CTCAACTTAC CTCATCTTCA GCGGAATACA AGACCTTCTC TGAGTAACTC TCAGAGGTTG
      * ***          *** * ****          * ** * * * * ****
137 : CAAAAC---- ---GTT- GAGGAA---- ----- -GGGT-TGTA TGAAAGGT--

301 : AAATGGGTAC CTTCAAGGAA GTTTATATCT ATGTTTCCTT CATGTGGTAT GCTAA--ACG
      *** * * ** **      *** * * * * ** * * * * * * * *
169 : AAAGGTGGAC CT-----GAA AATGGGATTT GTGACT-ATA CAGGAGTTAG ACAGAGGACA

359 : TGAATGCTCA GCCTAGTGTT CACATAATCC AGCAAAGACT AGAAGAACTC AAGAAAACCTG
      ** * * *      ** * * **      *** * * *      ** * ** ***
223 : TG--GGGTAA ATGGGTTGCT GAGATCCGTG AGCCAGGCC- -GAGGTGCT- AAG-----

419 : GACTTTTATC TCAATCCTAT TCTTCTAGTT CTTCTCCAC CGAATCAAAA ACTAATACTA
      * * * * * * * * * * * * * * * *          * * * * *
271 : ---TTATGGC TCGGTACT-T TC-TCTAGTT C----- ---ATATGAA GCT-GCATTG

479 : GCTTTCTTGA TGAGAAGACC AGCAAGGGAG AAACAGACAA TATGTTCGAA GGTGGTGATC
      ****   *** ****   ** * *** *      ** * ** * ** ***   *
313 : GCTT--ATGA TGAGGCTTCC A--AAGCTAT TTACGGTCAG TCTGCCGA- -----C

539 : AGAAGAAACC AGAGATCGAC CTGACCGAGT TTCTTCAGCA ACTAGGAATC TTGAAGGATG
      * * * * * * * *      *** **          * * * * * * * *
359 : TCAATCTTCC ACTGCTGCCA CTGTGTCAG- --GCTCGGTT ACT--GCATT TT--CTGATG

599 : AAAATGAAGC AGAACCAAGT GAGGTAGCAG AGTGTCTTTC CCCTCCACCA TGAACGAGC
      ** *****      ** ** *****          **          **   * **
412 : AATCTGAAGT TTGTGCACGT GAGG----- -----AT-- -----AC-- -----AAATGC

659 : AAGAAGAAAC TGGAAGTCCT TTCAGAACTG AGAATTTGAG CTGGGATACC CTGATCGAGA
      *** * * ***      * ** * * * ** * * *          ** ** ***
446 : AAG----ATC TGG-----T TTTGG---TC AG-ATCTC-- -----TA-A CTTCTCGCAT

```

Fig. 4-39

```

                                -0010181
719 : TGCCAAGAAG TGAACCACA ACTATGCAAT TTGACTCCAG CAACTTCGGA AGCTATGATT
    * ****          ***      * * * ****      ****      **      ***
483 : TTCCAA----- --AATG---- TTAAGTCCAA TAACT----- -GC----ATT

779 : TTGAGGATGA TGTATCCTTC CCTTCCATCT GGGACTACTA CGGAAGCTTA GATTGA
    * * * **          * * * * * * *      * * *
513 : -----GGTTA AGT-----T GGGGC-GTTA C-----TA G-----

```

+++++

```

Sequence 1      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+         : 2

Matching     : 38.38 [%]
Weight      : 325

```

```

1 : ATGGAAGAAG AGCAACCTCC GGCCAAGAAA CGAAACATGG GGAGATCTAG AAAAGGTTGC
  **          * * * * * * * * * * * * * * * * * * * * * * *
1 : AT----- GCCCAGGAAA CGGAAGTCTC GTGGAAC-AC GAGATGTAGC

61 : ATGAAAGGTA AAGGCGGTCC AGAGAACGCC ACGTGTACTT TCCGTGGAGT TAGGCAACGG
   *** *      **** *      *****      * * * * * * * * * * *
42 : -TGAGATTCT AAGGAAATGG AGAGA----- ----GTACAA TGAGCAGACC GAGGCA---G

121 : ACT-TGGGGT AAATGGGTGG CTGAGATCCG TGAGCCTAAC CGTGGGACTC GTCTCTGGCT
   * * * * * ** ***** ** * * * * * * * * * * * * * * *
89 : ATTCTTGCAT CGAT-GGTGG -TG-GTTC-- AAAACCAATC CGAAAGGCTC -----CT

180 : CGGCACGTTT AATACCTCGG TCGAGGCCGC CATGGCTTAC GATGAAGCCG CTAAGAAACT
   * **      ** ** ***** * * * * * * * * * * * * * * *
136 : C--CA----- AA----ACGT TCGAGG---- -AAGGGTT-- -----GTATGAAA--

240 : CTATGGACAC GAGGCTAAAC TCAACTTGGT GCACCCACAA CAACAACAAC AAGTAGTAGT
           * ****          *** * * *
166 : ----- --GGTAAA- -----GGT GGACC----- -----T

300 : GAACAGAAAC TTGTCTTTT CTGCCACCGG GTCGGGTTCT TGGGCTTATA ATAAGAAGCT
   **      ***          *** * * * * * * * * * * * * * * *
181 : GA----AAA- ----- --TGGGAT-T TGTGACTATA --CAGGAGTT

360 : CGATATGGTT CATGGGTTGG ACCTTGGTCT CGGCCAGGCA AGTTGTTTAC GAGGTTCTTG
   ** * *      ***** * * * * * * * * * * * * * * *
211 : AGACAGAGGA CATGGGGTAA A---TGG--- ----- -GTTGCT--- GAGATCCGTG

420 : CTCAGAGAGA TCGAGTTTTC TACAAGAAGA TGATGATCAT AGTCATAATC GATGTTCTGC
   ** **      ****          * * * * * * * * * * *
251 : ---AGCCAGG CCGAG----- ----- -GTGCTAA-- ---GTT----

480 : TTCAAGTGGT TCGAATCTTT GTTGGTTATT ACCTAAACAA AGTGATTCAC AAGATCAAGA

```

Fig. 4-40

-0010181

```

273 :   ***   ***   ****   *           ***
      -----ATGGC TCGGTACTTT CT----- --CTA-----

540 :   GACCGTTAAT GCTACGACTA GTTATGGCGG TGAAGGCGGT GGTGGCTCTA CGTTAACGTT
      *** *           ****           * * *   ***** ** * * * *
293 :   ---GTTCA- ----- --TATG---- ---AAGCTGC ATTGGCT-TA TGATGAGGCT

600 :   TTCGACCAAT TTGAAACCAA AGAATTTGAT GAGTCAGAAT TATGGATTAT ACAATGGAGC
      *           **** **   ** * *   ***** * **   *   **** *
328 :   T----- --CCAA AGCTATTTAC G-GTCAG--- TCTGCCCGAC TCAAT----C

660 :   TTGGTCTAGG TTTCTTGTGG GGCAAGAAAA GAAGACGGAA CATGACGTGT CATCGTCGTG
      ** ** * * *   ** * * *   ***           * ** **   *** **
365 :   TTCCACT--G CTGCCACTGT GTCAGG---- ---CTCGG-- --TTAC-TG- CATTTTCTGA

720 :   TGGATCGTCG GACAACAAGG AGAGTATGTT GGTTCCTAGT TGCGGCGGAG AGAGGATGCA
      ** ***           * * *** ***           ** *   ***** **
410 :   TGAATC---- -----TG A-AGTTTGT- ----- ----GC-ACG TGAGGATACA

780 :   TAGGCCGGAG TTGGAAGAGC GAACAGGATA TTTGGAAATG GATGATCTTT TGGAGATTGA
      *           ** **** *           ** *   *** *** * **
441 :   AA----- -TGCAAGATC -----TG G-----TTT TGGTCA--GA

840 :   TGATTTAGGT TTGTTGATTG GCAAAAATGG AGATTTCAAG AATTGGTGTT GTGAAGAGTT
      * * **   ** * * *   *   ***** * * *** ** ** *   ** ***
466 :   T-CTCTA-AC TTCTCGCATT TCCAAAATGT TAAGTCCAAT AACTGCATTG GTTAAG----

900 :   TCAACATCCA TGGAATTGGT TCTGA
      * *   * * **
520 :   ----- TTGGGGCGTT ACTAG

```

Fig. 5-1

0056504

+++++

Sequence 1 : DREB2A.aa
 Size : 335
 Matching Position : 1 - 335

Sequence 2 : DREB2B.aa
 Size : 330
 Matching Position : 1 - 330

Matching Condition.

Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2
 Matching : 53.30 [%]
 Weight : 6

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVE--- --EVSTKKRK
    **** *      *      * **** * * *** ** * **** *      * ***
1 : MAVYEQ---- --TGTEQPKK RKSRRARAGGL TVADRLKKWK EYNEIVEASA VKEGKPKRK

56 : VPAKGSKKGC MKGKGGPENS RCSFRGVRQR IWGKWVAEIR EPNRGSRLWL GTFPTAQEAA
    ***** ** ***** ** ***** ** ***** ** * **** ***** **
55 : VPAKGSKKGC MKGKGGPENS HCSFRGVRQR IWGKWVAEIR EPKIGTRLWL GTFPTAEKAA

116 : SAYDEAAKAM YGPLARLNFP RSDASEVTST SSQSEVCTVE ----TPGCVH VKTEDPDCES
    ***** ** ** ***** * ** *** ***** ** * ** ** ** ****
115 : SAYDEAATAM YGSLARLNFP QSVGSEFTST SSQSEVCTVE NKAIVCGDVC VKHEDTDCES

172 : KPF----- --SGGVEPMY CLENGAEEMK RGVKADKHWL SEFEHNYWSD ILKEKEKQK-
    **      * * *      * * *      * * *      * * *      * **** *
175 : NPFSQILDVR EESCGRTPDS C-TVGHQDMN SSLNYD--LL LEFEQQYWGQ VLQEKEKPKQ

222 : -----EQGIV ETCQQQ-QQD SLSVADYGWP --ND--VDQS HLDSSDMFDV DELLRLNGD
    *      * * * * * * ***** ** ** *      *      *      *
232 : EEEEIQQQQQ EQQQQLQPD LLTVADYGWP WSNDIVNDQT SWDPNECFDI NELLGDLN--

272 : DVFAGLNQDR YPGNSVANGS YRPESQQSGF DPLQSLNYGI PPFQLEGKDG NGFFDDLSTYL
    * *      * * *      *      *      *      *      *      *      *
290 : --EPGPHQ-S QDQNHVNSGS -----YDL HPLHLEPHDG -HEFNGLSSL

332 : DLEN
    *
329 : D--I

```

+++++

Sequence 1 : DREB2A.aa
 Size : 335
 Matching Position : 1 - 335

Sequence 2 : DREB2C.aa
 Size : 341
 Matching Position : 1 - 341

Matching Condition.

Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2

Fig. 5-2

0056504

Matching : 36.83 [%]
Weight : 128

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS -----TKK
  *          ** **** *      *** * *      **** * *
1 : M----- --PSEIVDRK RKSRTGRD-- -VAEILRQWR EYNEQIEAES CIDGGGPKSI

54 : RKPVPAGSKK GCMKGKGPE NSRCSFRGVR QRIWGKWVAE IREPNRGSR L WLGTFPTAQE
  ** * *** * ***** * * **** ** ***** **** * ** ***** *
47 : RKPPPKGSRK GCMKGKGPE NGICDYRGVR QRRWGKWVAE IREPDDGAR L WLGTFSSSYE

114 : AASAYDEAAK AMYGPLARLN FPRSDASEVT STSSQSEVCT VETPGCV--- HVKTEDPDCE
  ** ***** * ** **** * * * * * * * * * * * *
107 : AALAYDEAAK AIYQGSARLN LP-----EIT NRSS--STAAT ATVSGSVTAF SDESEVCARE

171 : SKPFSGGVEP MYCLENAAE MKRGVKADKH WLSEFEHNYW SDILKEKEKQ KEQGIVETCQ
  * *          ** *      * *      *      ** ** *
161 : DTNASSG-FG QVKLEDCSDE ---YVLLDSS QCIKEE---- ---LKGKEEV REEHNLA VGF

231 : QQQQDS---- LSVADYGWP N DVDQSHLDSS DMFDVDELLR DLNGDDV--- -FAGLNQDRY
  *** *      * *      ** *** ** *      **
210 : GIGQDSKRET LDAWLMGNGN EQEPLEFGVD ETFDINELLG ILNDNNVSGQ ETMQYQVDRH

283 : P-----G NSVANGSYRP -ESQQSGFD- -----PLQS LNYGIPPFQL EGKD---GNG
  *      ** * * * * * *      *      **** *
270 : PNFSYQTQFP NSNLLGSLNP MEIAQPGVDY GCPYVQPSDM ENYGIDLDHR RFNDLDIQDL

324 : FFDDL SYLDL EN
  *
330 : DFGGDKDVHG ST

```

+++++

Sequence 1 : DREB2A.aa
Size : 335
Matching Position : 1 - 335

Sequence 2 : DREB2D.aa
Size : 206
Matching Position : 1 - 206

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*Nt : 2

Matching : 28.96 [%]
Weight : 167

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  *          *      * *      *      * * *
1 : M----- -----SSIE PKVMMVG--- -----AN KKQRTVQA-S

61 : SKKGCMKGKG GPENSRCFR GVRQRIWGKW VAEIREPNRG SRLWLGTFPT AQEAASAYDE
  * **** *** ** * *      ***** **** ***** **** * * * *
24 : SRKGCMRGKG GPDNASCTYK GVRQRTWGKW VAEIREPNRG ARLWLGTFDT SREAALAYDS

121 : AAKAMYGLA RLNFPRSDAS EVTSTSSQSE VCTVETPGCV HVKTEDPDCE SKPFSGGVEP
  ** *** * ** * *      **      **      * * * *

```

Fig. 5-3

0056504

```

84 : AARKLYGPEA HLNLPESLRS YPKTASS--- PASQTPSSN TGGKSSSDSE S-PCS-----
181 : MYCLENAGEE MKRGVKADKH WLSEFEHNYW SDILKEKEKQ KEQGIVETCQ QQQQDSLSVA
      * * * * *
135 : -----SNE M-----S SCGRVTEEIS WEHINV---- ----DLPVM

241 : DYGWPNDVDQ SHLDSSDMFD VDELLRDLNG DDVFAGLNQD RYPGNSVANG SYRPESQQSG
      * * * * *
161 : D-----DSS---I WEEATMSLGF PWVHEGDN-- ----DISR

301 : FDPLQSLNYG IPPFQLEGKD GNGFFDDLSY LDLEN
      * * * * *
188 : FDTCLIS---- ----GGYSNWDSFH SPL--
  
```

+++++

```

Sequence 1      : DREB2A.aa
Size            : 335
Matching Position : 1 - 335
  
```

```

Sequence 2      : DREB2E.aa
Size            : 244
Matching Position : 1 - 244
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 34.20 [%]
Weight       : 143
  
```

```

1 : MAYVDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  * * * * *
1 : MEKEDNGSKQ SSSASVSSR ---RRRRVVE PVEATLQRW- ----EEGL ARARRVQAKG

61 : SKKGCMKGKG GPENSRCSEFR GVRQRIWGKW VAEIREP--- ----NRGSR LWLGTFTAQ
***** * * * * *
52 : SKKGCMRGKG GPENPVCSEFR GVRQRVWGKW VAEIREPVSH RGANSRSKR LWLGTFTAA

113 : EAASAYDEAA KAMYGPLARL NFPRSDASEV TSTSSQSEVC TVETPGCVHV KTEDPDCESE
*** * * * *
112 : EAALAYDRAA SVMYGPYARL NFP----- --EDLGGGRK K--DEEAES-

173 : PFSGGVEPMY CLE-NGAEEM KRGVKADKHW LSEFEHNYWS DILKEKEKQK EQGIVETCQ
*** * * * *
150 : --SGG----Y WLETNKA--- GNGV----- --IETEGGK DYVVYNEDAI ELGHDKT-QN

232 : QQQDSLSVAD YGWPNDVDQS HLDSSDMFDV DELLRLDNGD DVFAGLNQDR YPGNSVANGS
  * * * * *
191 : PMTDNEIV-- ---NPAVKSE EGYSYDRFKL D----- ----NGL

292 : YRPESQQSGF DPLQSLNYGI IPPFQLEGKD GNGFFDDLSY- LDLEN
  * * * * *
220 : LYNEPQSS-- ----SYHQG- ----GGFD--SYF EYFRF
  
```

+++++

```

Sequence 1      : DREB2A.aa
Size            : 335
Matching Position : 1 - 335
  
```

Fig. 5-4

0056504

Sequence 2 : DREB2F.aa
Size : 277
Matching Position : 1 - 277

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 27.71 [%]
Weight : 176

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  *          *          *          *          *
1 : M----- EKSS-----MKQ

61 : SKKGCMKGGK GPENSRCFSR GVRQRIWGKW VAEIREPNRG SRLWLGTFPT AQEAASAYDE
    *** ** * * * ***** **
10 : WKKGPARGKG GPQNALCQYR GVRQRTWGKW VAEIREPKKR ARLWLGSFAT AEEAAMAYDE

121 : AAKAMYGPLA RLNFPRSDAS EVTSTS-SQ- ----SEVCT VETPGC---- ----VHVKTE
    ** ** * ** * * ** * *
70 : AALKLYGHDA YLNLPHLQRN TRPSLSNSQR FKWVPSRKFI SMFPSCGMLN VNAQPSVHII

166 : DPDCESKPFS GGVEPMYCLE NGAEMKRGV KADKHWLSEF EHNYWSDILK EKEKQKEQGI
    *          *          *          *          *
130 : QQRLEELKKT GLLSQSYSSS SSSTE----S KTNTSFLDEK TSKGETDNMF EGGDQKKPEI

226 : VETCQQQQQD SLSVADYGWP NDVDQSHLDS SDMFDVDELL RDLNGDDVFA GLNQDRYPGN
    * ** * * * *
186 : DLTEFLQQLG ILKDENEAP SEVAECH--S PPPWNEQEET GSPFRTENFS WDTLIEMP--

286 : SVANGSYRPE SQQSGFDPLQ SLNYGIPPFQ LEGKDGNGFF DDLSYLDLEN
    * * ** * * *
242 : -----RSE TTMQFD--- SSNFGSYDF- ---EDDVSFP SIWDYYGSLD

```

+++++

Sequence 1 : DREB2A.aa
Size : 335
Matching Position : 1 - 335

Sequence 2 : DREB2G.aa
Size : 306
Matching Position : 1 - 306

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 26.12 [%]
Weight : 184

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  *          *          *          *          *
1 : -----EEEQ PPAKKRNMGR

61 : SKKGCMKGGK GPENSRCFSR GVRQRIWGKW VAEIREPNRG SRLWLGTFPT AQEAASAYDE

```

Fig. 5-5

```

                                0056504
15 : * ***** **** * ** ***** **** ***** ***** * *** ****
      SRKGCMKGKG GPENATCTFR GVRQRTWGWK VAEIREPNRG TRLWLGTFNT SVEAAMAYDE

121 : AAKAMYGPLA RLN--FPRSD ASEV----TS TSSQSEVCTV ETPGCVHVKT EDPDCESKPF
      *** ** * ** * * * * * * *
75 : AAKKLYGHEA KLNLYHPQQQ QVVVNRNLS FSGHSGSWA YNKKLDMVHG LDLGLGQASC

175 : SGGVEPMYCL ENGAEEMKRG VKADKHWLSE FEHNYWSDIL KEKEKQKEQG IVETCQQQQQ
      * * * * * * * * * * * *
135 : SRG----SCS ERSSFLQEDD DHSHNRCSSS SGSNLCWLLP KQSDSQDQET VNATTSYGGE

235 : DLSLSVADYGW PNDVDQSHLD SSDMFDVDEL LRDNLGDDVF AGLNQDRYPG NSVANGS---
      * * * * * * *
191 : GGGGSTLTFS TNLKPKNLMS QNYGLYNGAW SRFLVGQEKK TEHDVSSSCG SSDNKESMLV

292 : -----YR PE-SQQSGFD PLQSLNYGIP PFQLEGKDG- --NGFFDDL S YLDLEN
      * ** * * * * * *
251 : PSCGGERMHR PELEERTGYL EMDDLLEIDD LGLLIGKNGD FKNWCCEEFQ HPWNWF

+++++

Sequence 1 : DREB2A.aa
Size : 335
Matching Position : 1 - 335

Sequence 2 : DREB2H.aa
Size : 177
Matching Position : 1 - 177

Matching Condition.

Matches : -1
Mismatch : 1
Gaps : 1
* N+ : 2

Matching : 28.07 [%]
Weight : 170

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVE--- ----EVSTKK
      * ** **** * *** * * **** *
1 : M-----PRK RKSRTGRD--VAEILRKWR EYNEQTEADS CIDGGGSKPI

54 : RKVPAKGSKK GCMKGKGPE NSRCSFRGVR QRIWGWVAE IREPNRGSRL WLGTFTAQAE
      ** * * * ***** * * *** ** ***** **** * * *
42 : RKAPPKRSRK GCMKGKGPE NGICDYTGVR QRTWGWVAE IREPGRGAKL WLGTFSSES

114 : AASAYDEAAK AMYGPLARLN FPRSDASEVT STSSQSEVCT VETPGCVHVK TEDPDCESKP
      ** ***** * ** **** * *
102 : AALAYDEASK AIYGQSARLN LP----- -LLPLC---

174 : FSGGVEPMYC LENGAEEMKR GVKADKHWLS EFEHNYWSDI LKEKEKQKEQ GIVETCQQQQ
      * * * * *
129 : -----QARLL HFLMN---- LK----- -FVHVRIQM

234 : QDSLSVADYG WPNDVDQSHL DSSDMFDVDE LLRDNLGDDV FAGLNQDRYP GNSVANGSYR
      * * * * *
150 : DLVL----- -VRSLS RISKMLSPIT AL----- -VKLGRY-

294 : PESQQSGFDP LQSLNYGIPP FQLEGKDGNG FFDDL SYLDL EN
178 : -----

```


Fig. 5-6

0056504

+++++

Sequence 1 : DREB2B.aa
 Size : 330
 Matching Position : 1 - 330

Sequence 2 : DREB2C.aa
 Size : 341
 Matching Position : 1 - 341

Matching Condition.

Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2

 Matching : 33.62 [%]
 Weight : 134

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PK--RKVPAK
  * ***** * ** * * **** ** * ** ** *
1 : M-----PSEI VDRKRKSR-- -GTRDVAEIL RQWREYNEQI EAESCIDGGG PKSIRKPPPK

59 : GSKKGCMKGK GGPDSHCSF RGVQRRIWGK WVAEI REPKI GTRLWLGTFP TAEKAASAYD
  ** ***** *** * * ***** *** ***** * ***** ** ***
53 : GSRKGCMKGK GGPENGICDY RGVQRRIWGK WVAEI REPDI GARLWLGTFS SSYEALAYD

119 : EAATAMYGSL ARLNFP---- ------QS VGSEFTSTSS QSEVCTVENK AVVCGDVCVK
  *** * ** **** * * * * * **** * * **
113 : EAAKAIYGQS ARLNLPEITN RSSSTAATAT VSGSVTAFSD ESEVCAREDT NASSGFGQVK

167 : HEDTDCESNP FSQILDVREE SCG----TRP DSCTVGHQDM NSSLNYDLLL EFEQQYWGQV
  ** * ** ** * ** * * *
173 : LEDCSDEYVL LDSSQCIKEE LKGKEEVREE HNLAVGFGIG QDSKRETLDA WLMGNGNEQE

223 : LQE---KEKP KQEE---EEI QQQQQEQQQQ QLQPDLLTVA DYGWPWSNDI VNDQTSWDPN
  * * * * * * * * * * * * *
233 : PLEFGVDETF DINELLGILN DNNVSGQETM QYQVDRHPNF SYQTQFPN-- SNLLGSLNPM

277 : ECFDINELLG DLNEPGPHQS QDQNHVNSGS YDLHPLHLEP HDGHEFNGLS SLDI
  * * * * *
291 : E---IAQPGV DYGCPYVQPS DMENYGIDLH HRRFNDLDIQ DLDFGGDKDV HGST

```

+++++

Sequence 1 : DREB2B.aa
 Size : 330
 Matching Position : 1 - 330

Sequence 2 : DREB2D.aa
 Size : 206
 Matching Position : 1 - 206

Matching Condition.

Matches : -1
 Mismatches : 1
 Gaps : 1
 *N+ : 2

 Matching : 28.48 [%]
 Weight : 166

Fig. 5-7

0056504

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPKGS
  * * * * *
1 : MSSIE----- -PK----- -VMMV GA-----NK KQRTVQA-SS

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGKVV AEIREPKIGT RLWLGTFPTA EKAASAYDEA
  **** * * * * *
25 : KKGCMRGKGG PDNASCTYKG VRQRTWGKVV AEIREPNRGA RLWLGTFDTS REAALAYDSA

121 : ATAMYGSLAR LNFPQSVGSE FTSTSSQSEV CTVENKAVVC GDVCVKHEDT DCESNPFQI
  * * * * *
85 : ARKLYGPEAH LNLPELSRSY PKTASS----- -PASQ-

181 : LDVREESCGT RPDSCVTGHQ DMNSSLNYDL LLEFEQQYWG QVLQEKEKPK QEEEEIQQQ
  * * * * *
115 : -----T TPSSNTGG-- -KSSSDSESP CSSNEMSSCG RV----- -TEEI-----

241 : QEQQQQQLQP DLLTVADYGW PWSNDIVNDQ TSWDPNECFD INELLGDLNE PGPHQSQDQN
  * * * * *
149 : ----SWEHIN VDLPMDDSS IWEEATMSLG FPWVHEGND I--SRFDTCI SGGYSNWDSF

301 : HVNSGSYDLH PLHLEPHDGH EFNGLSSLDI
  * * *
203 : H----- -SPL--

```

+++++

```

Sequence 1      : DREB2B.aa
Size            : 330
Matching Position : 1 - 330

Sequence 2      : DREB2E.aa
Size            : 244
Matching Position : 1 - 244

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

Matching         : 29.20 [%]
Weight          : 161

```

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPKGS
  * * * * *
1 : M-EKEDNG-- --SKQSSA- --SVVSSRRR RRVVEPVEAT LQRWEEGLA RARRVQAKGS

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGKVV AEIREP---- ----KIGTRL WLGTFTAEK
  **** * * * * *
53 : KKGCMRGKGG PENPVCFRG VRQRVWGKVV AEIREPVSHR GANSSRSKRL WLGTFTAAE

113 : AASAYDEAAT AMYGSLARLN FPQSVGSEFT STSSQSEVCT VENKAVVCGD VCVKHEDTDC
  ** *** ** *** **
113 : AALAYDRAAS VMYGPYARLN FP----- -

173 : ESNPFSQILD VREESCGTRP DSCTVGHQDM NSSLNYDLLL EFEQQYWGQV LQEKEKPKQE
  * * * * *
135 : EDLGGGRKGD EEAESSG--- -----GYWL ETNKAGNGVI ETEGGKDYVV

233 : EEEIQQQQQE QQQQLQPD LTVADYGPW SNDIVNDQTS WDPNECFDIN ELLGDLNEPG

```

Fig. 5-8

```

                                0056504
                                *   *   *
176 : YNEDAIELGH DKTQNPMTD- ----- -NEIVNPAVK SEEGYSYDRF KLDNGL----
                                *   *   *
293 : PHQSQDQNHV NSGSYDLHPL HLEPHDGEF -NGLSSLDI
                                *   *   *
220 : -----LYNEP QSSSY----- ----HQGGGF DSYFEYFRF

```

+++++

```

Sequence 1      : DREB2B.aa
Size            : 330
Matching Position : 1 - 330

```

```

Sequence 2      : DREB2F.aa
Size            : 277
Matching Position : 1 - 277

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*Nt          : 2

Matching      : 28.06 [%]
Weight       : 163

```

```

1 : MAVYEQTGTE QPKKRKSRR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPKGS
  *----- **
1 : M-----EK ---SSMKQW

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGKVV AEIREPKIGT RLWLGTFPTA EKAASAYDEA
    *** **** * * * ** ***** ***** ***** * * * * *
11 : KKGPARCKGG PQNALCQYRG VRQRTWGKVV AEIREPKKRA RLWLGSFATA EEAAMAYDEA

121 : ATAMYGSLAR LNFPQSVGSE FTSTS-SQSE VCTVENKAVV CGDVCVKHED TDCESNPFSSQ
    * ** * ** * * * * * * * * * *
71 : ALKLYGHDAY LNLPHLQRNT RPSLSNSQRF KWVPSRKFI MFPSCGMLNV NAQPSVHI IQ

180 : ILDVREESCG TRPDCTVGH QDMNSSLNYD LLEFEQQYW GQVLQEKEKP KQEEEEIQQQ
    * * * * * * * * * *
131 : QRLEELKKTG LLSQSYSSSS SITESKTNTS FL--DEKTSK GETDNMFEGG DQKKPEIDLT

240 : QQEQQQQQL- ---QPDLLTV ADYGWPWSND IVNDQTSWDP NECFDINELL GDLNEPGPHQ
    ** * * * * * * *
189 : EFLQLGLK DENEAPSEV AECHSPPPWN EQEETGSPFR TENFSWDTLI EMRSETTTM

296 : SQDQNHVNSG SYDLHPLHLE PHDGEFNGL SSLDI
    * * * * *
249 : QFD--SSNFG SYDFEDDVSF P---SIWDYY GSLD-

```

+++++

```

Sequence 1      : DREB2B.aa
Size            : 330
Matching Position : 1 - 330

```

```

Sequence 2      : DREB2G.aa
Size            : 306
Matching Position : 1 - 306

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1

```

Fig. 5-9

0056504

```

Gaps          :      1
*Nt           :      2

Matching      :    26.35 [%]
Weight        :    185

```

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPAGKS
   * **
1 : -----EEE QP-----
   PAKKRNMGRS

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGWV AEIREPKIGT RLWLGTFTA EKAASAYDEA
    ***** * * * *** **** * ** * ** * ** * ** * ** *
16 : RKGCMKGKGG PENATCTFRG VRQRTWGWV AEIREPNRGT RLWLGTFTS VEAAMAYDEA

121 : ATAMYGLAR LN--FPQSVG SEFTSTSSQS EVCTVENKAV VCGDVCVKHE DTDCEPNPFS
    * ** * ** ** *
76 : AKKLYGHEAK LNLVHPQQQ QVVVNRNLSF SGHSGSWAY NKKLDMVHGL DLGLGQASCS

179 : QILDVREESC GTRPDSCTVG HQDMNSSLNY DLLLEFEQY WGQVLQEKEK PKQEEEEIQ
    * * * * * * * * * *
136 : -RGSCSERSS FLQED-DDHS HNRCSSSSGS NLCWLLPKQS DSQDQETVNA TTSYGGEGGG

239 : QQEQQQQQQL QPDLLTVADY G---WPWS-- -----N DIVNDQTSWD PNECFDINEL
    * * * * * ** * * *
194 : GSTLTFTSNL KPNLMSQNY GLYNGAWSRF LVGQEKKEH DVSSSCGSSD NKESMLVPSC

285 : LG---DLNEP GPHQSQDQNH VNSGSYDLHP LHLEPHD--- -GHEFNLSS LDI
    * * * ** * *
254 : GGERMHRPEL EERTGYLEMD DLLEIDDLGL LIGKNGDFKN WCCEEFQHPW NWF

```

+++++

```

Sequence 1      : DREB2B.aa
Size            :    330
Matching Position :    1 - 330

```

```

Sequence 2      : DREB2H.aa
Size            :    177
Matching Position :    1 - 177

```

Matching Condition.

```

Matches        :    -1
Mismatches     :     1
Gaps           :     1
*Nt            :     2

Matching       :    28.92 [%]
Weight        :    160

```

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EA--SAVKEG EPKRKVPAGK
   * * * * * * * * *
1 : M----- -PRKRKSR-- -GTRDVAEIL RKWREYNEQT EADSCIDGGG SKPIRKAPKP

59 : GSKKGCMKGK GGPDSHCSF RGVRQRIWGW WVAEIREPKI GTRLWLGTFT TAEKAASAYD
   * * * * * * * * * *
48 : RSRKGCMKGK GGPENGICDY TGVQRWGW WVAEIREPGR GAKLWLGTFS SSYEALAYD

119 : EAATAMYGL ARLNFPQSVG SEFTSTSSQS EVCTVENKAV VCGDVCVKHE DTDCEPNPFS
    * * * * *
108 : EASKAIYGQS ARLNLP-----

```

Fig. 5-10

```

                                -0056504
179 : QILDVREESC GTRPDSCTVG HQDMNSSLNY DLLLEFEQQY WGQVLQEKEK PKQEEEEIQQ
124 : ----- --LLPLCQ-- -ARLLHFLMN LKFVHVRIQM

239 : QQQEQQQQL QPDLTVADY GWPWSNDIVN DQTSWDPNEC FDINELLGDL NEPGPHQSQD
149 : Q----- --DL----- -VLVR SLTS----- -RISKML--- -----SPI

299 : QNHVNSGSYD LHPLHLEPHD GHEFNGLSSL DI
169 : TALVKLGRY- -----

```

+++++

```

Sequence 1      : DREB2C.aa
Size           : 341
Matching Position : 1 - 341

```

```

Sequence 2      : DREB2D.aa
Size           : 206
Matching Position : 1 - 206

```

Matching Condition.

```

Matches       : -1
Mismatches    : 1
Gaps          : 1
*N+           : 2

Matching      : 29.03 [%]
Weight       : 167

```

```

1 : MPSEIVDRKR KSRGTRDAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PKGSRKGCMMK
* * * * *
1 : MSS----- -IEPKVMMVG ANKK--QRTV QASSRKGCMMR

61 : GKGGPENGIC DYRGVRQRRW GKWVAEIREP DGGARLWLGT FSSSYEAALA YDEAAKAIYG
***** * * * *
31 : GKGGPDNASC TYKGVQRQRTW GKWVAEIREP NRGARLWLGT FDTsREAALA YDSAARKLYG

121 : QSARLNLPEI TNRSSSTAAT ATVSGSVTAF SDESEVCARE DTNASSGFGQ VKLEDSCSDEY
* * * * *
91 : PEHLNLPE- ----- SLRSYPKTAS SPAS----- QTPSSNTG- --GKSSSD--

181 : VLLDSSQCIK EELKGKEEVR EEHNLA VGFG IGQDSKRETL DAWLMGNGNE QEPLFVGDE
* * * * *
129 : ---SESPCSS NEMSSCGRVT EE----- -----IS

241 : TFDINELLGI LNDNNVSGQE TMQYQVDRHP NFSYQTQFPN SNLLGSLNPM EIAQPGVDYG
* * * * *
150 : WEHINVDPV MDDSSIWEEA TM----- -SL-----G

301 : CPYVQPSDME NYGIDLHRR FNDLDIQDLD FGDKDVHGS T
* * * * *
175 : FPWV----- -HEGDNDISR F-DTCISGGY SNWD-SFHSP L

```

+++++

```

Sequence 1      : DREB2C.aa
Size           : 341
Matching Position : 1 - 341

```

Fig. 5-11

0056504

Sequence 2 : DREB2E.aa
Size : 244
Matching Position : 1 - 244

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 30.29 [%]
Weight : 172

```

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEA-ESCID GGGPKSIRKP PPKGSRKGC
  * * * * *
1 : MEKEDNGSKQ SS---SASVV SSRRRRRVVE PVEATLQRWE EEGLARARRV QAKGSKKGC

60 : KGKGGPENG I CDYRGVRQRR WGKWVAEIRE P--DGG A--- ---RLWLGT F SSSYEAAALAY
  * * * * *
58 : RGKGGPENPV CRFRGVRQRV WGKWVAEIRE PVSHRGANSS RSKRLWLGT F ATAAEAALAY

112 : DEAAKAIYGQ SARLNLPEIT NRSSSTAATA TVSGSVTAFS DESEVCARED TNASSGFGQV
  * * * * *
118 : DRAASVMYGP YARLNFPE-- ----- -DLGGGRKKD EEAE----- ---SSG---

172 : KLEDSCSEYV LLDSSQCIKE ELKGKEEVRE EHNLA VGFGI GQDSKRETLD AWLMGNGNEQ
  * * * * *
152 : -----GYW L----- ETNKA---GN G---VIETEG GKDYVVYNE-

232 : EPLEFGVDET FDINELLGIL NDNNVSGQET MQYQVDRHPN FSYQTQFPNS NLLGSLNPME
  * * * * *
179 : DAIELGHDKT QNPMTDNEIV NPAVKS---E EGYSYDR--- -----FKLD N-----

292 : IAQPGVDYGC PYVQPSDMEN YGIDLHRRF NDLDIQDLDF GGDKDVHGST
  * * * * *
218 : ----GLLYNE P--QSSSYHQ GG----- ----GFDSYF ----EYFRF
  
```

+++++

Sequence 1 : DREB2C.aa
Size : 341
Matching Position : 1 - 341

Sequence 2 : DREB2F.aa
Size : 277
Matching Position : 1 - 277

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 29.89 [%]
Weight : 172

```

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PKGSRKGC
  * * * * *
1 : M----- --EKS---SS MKQWKGPAP

61 : KGKGGPENG I C DYRGVRQRRW GKWVAEIREP DGGARLWLGT FSSSYEAAAL YDEAAKAIYG
  * * * * *
  
```

Fig. 5-12

-0056504

```

17 : GKGGPQNALC QYRGVRQRTW GKWVAEIREP KKRARLWLGS FATAEEAAMA YDEAALKLYG

121 : QSARLNL-- -EITNRSSST AATATVSGSV TAFSDESEVC AREDTNA--S SGFGQVKLED
      * ****      * * *      * * *      * * *      * * *
77 : HDAYLNLPHL QRNTRPSLSN SQRFKWVPS- RKFISMFPSC GMLNVNAQPS VHIIQRLE-

176 : CSDEYVLLDS SQCIKEELKG KEEVREEHNL AVGFGIGQDS KRETLDALWM GNGNEQEPL
      ** **      * *      * *      * * *      * * *
135 : ELKKTGLL-- SQ-----SYS SSSSSTESKT NTSFLDEKTS KGET---DNM FEGGDQKKPE

236 : FGVDETFDIN ELLGILNDNN VSGQETMQYQ V-DRHPNFSY QTQFPNSNLL GSLNPMEIAQ
      * *      **** * *      * *      * *      * *
185 : --IDLT-EFL QQLGILKDEN ----EAEPSE VAECHSPPPW NEQ----EET GSPFRTENFS

295 : PGVDYGCPYV QPSDMENYGI DLDHRRFNDL DIQDLDFGGD KDVHGS-T
      * *      * *      * *      * *      * *
234 : WDTLIEMPRS ETTMQFDSS NFGSYDFED- ---DVSFPSI WDYYGSLD
  
```

+++++

```

Sequence 1      : DREB2C.aa
Size            : 341
Matching Position : 1 - 341
  
```

```

Sequence 2      : DREB2G.aa
Size            : 306
Matching Position : 1 - 306
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 28.25 [%]
Weight       : 174
  
```

```

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PKGSRKGCMK
      * * *      * * *      * * *
1 : -----EEE QPPA-----KKNR MGRSRKGCMK

61 : GKGGPENGIC DYRGVRQRRW GKWVAEIREP DGGARLWLGT FSSSYEAALA YDEAAKAIYG
      * * *      * * *      * * *      * * *      * * *
22 : GKGGPENATC TFRGVRQRTW GKWVAEIREP NRGTRLWLGT FNTSVEAAMA YDEAAKKLYG

121 : QSARLNL--- ----PEITNR SSSTAATATV SGSVTAFSDE SEVCAREDTN ASSFGQVKL
      * * *      * *      * *      * *      * *
82 : HEAKLNLVHP QQQQVVVNR NLSFSGHGSG SWAYNKKLDM VHGLDLGLGQ ASCSRG-SCS

174 : EDCSDEYVLL DSSQCIKEEL KGKEEVREEH NLAVGFGIGQ DS-KRETLD --WLMGNGNE
      * *      * *      * *      * *      * *
141 : ERSFQLQEDD DHSHNRCSSS SG-----S NLCWLLPKQS DSQDQETVNA TTSYGEGGG

231 : QEPLEF-GVD ETFDINELLG ILNDNNVSGQ ETMQYQVDRH PNFSYQTFP N--SNLLGSL
      * *      * *      * *      * *      * *
194 : GSTLTFSTNL KPNLMSQNY GLYNGAWSRF LVGQEKTEH DVSSSCGSSD NKESMLVPSC

288 : NPMEIAQPGV DYGCPIYVQPS DMENYIDLD HRRFNDLDIQ DLDFGGDKDV HGST
      * *      * *      * *      * *
254 : GGERMHRPEL EERTGY-LEM DDLLEIDDLG LLIKNGDFK NWCCEEFQHP WNW
  
```

Fig. 5-13

0056504

+++++

Sequence 1 : DREB2C.aa
Size : 341
Matching Position : 1 - 341

Sequence 2 : DREB2H.aa
Size : 177
Matching Position : 1 - 177

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 38.42 [%]
Weight : 97

```

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PKGSRKGCMK
  ** *** ***** * * * * * * * * * * * * * * * * * * * * * * *
1 : MP-----RKR KSRGTRDVAE ILRKWREYNE QTEADSCIDG GSKPIRKAP PKRSRKGCMK

61 : GKGGPENGIC DYRGVRQRRW GKWVAEIREP DGGARLWLGT FSSSYEAALA YDEAAKAIYG
  ***** ** * * * * * * * * * * * * * * * * * * * * * * *
56 : GKGGPENGIC DYTGVRQRTW GKWVAEIREP GRGAKLWLGT FSSSYEAALA YDEASKAIYG

121 : QSARLNLPEI TNRSSSTAAT ATVSGSVTAF SDESEVCARE DTNASSGFGQ VKLEDSCSEY
  *****
116 : QSARLNLPEI -----

181 : VLLDSSQCIC EELKGKEEVR EEHNLAVGFG IGQDSKRETL DAWLMGNGNE QEPLEFGVDE
  ** * * * * * * * * * * * * * * * * * * * * * * *
124 : -LLPLCQ--- ----- -ARL----- -LHF-----

241 : TFDINELLGI LNDNNVSGQE TMQYQVDRHP NFSYQTQFPN SNLLGSLNPM EIAQPGVDYG
  * * * * * * * * * * * * * * * * * * * * * * *
136 : -----LMN LKFVHVRIQ- MQDLV----- -LVRSL-----

301 : CPYVQPSDME NYGIDLDHRR FNDLDIQDLD FGGDKDVHGS T
  * * * * * * * * * * * * * * * * * * * * * * *
158 : --TSRISKM- -----LS PITALVKLGR Y
  
```

+++++

Sequence 1 : DREB2D.aa
Size : 206
Matching Position : 1 - 206

Sequence 2 : DREB2E.aa
Size : 244
Matching Position : 1 - 244

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 35.20 [%]
Weight : 96

Fig. 5-14

0056504

```

1 : M-----SS- -IEPKMMVG A----- NKKQRTVQA- SSRKGCMRGK
   *      **      * * *      * * *      * * *
1 : MEKEDNGSKQ SSSASVVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGCMRGK

33 : GGPDNASCTY KGVQRQRTWGK WVAEIREP-- NRGA----- RLWLGTFDTS REAALAYDSA
   *** * *      ***** **      ***      ***** *      ***** *
61 : GGPENPVCRF RGVQRQVWGK WVAEIREPVS HRGANSSRSK RLWLGTFATA AEAALAYDRA

85 : ARKLYGPEAH LNLPELSRSY PKTASSPASQ TTPSSNTGGK SSSDSESPCS SNEMSSCGRV
   *   *** *   ** * *   *   *   *   *   *   *   *   *   *
121 : ASVMYGPYAR LNFPEDLGGG RKKDEEAESS GGYWLETNKA GNGVIE---- -TEGGKDYVV

145 : TEE--ISWEH INVDPVMDD SSIWEEATMS --LGFPPVHE GDNDISRFDT CIS----GGY
   * * *   * * *   * * *   * * *   * * *   * * *   * * *
176 : YNEDAIELGH DKTQNP-MTD NEIVNPAVKS EEGYSYDRFK LDNGLLYNPE QSSSYHQGGG

197 : SNWDSFHSPL

235 : FDSYFEYFRF

```

+++++

```

Sequence 1      : DREB2D.aa
Size            : 206
Matching Position : 1 - 206

Sequence 2      : DREB2F.aa
Size            : 277
Matching Position : 1 - 277

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*Nt.        : 2

Matching      : 32.65 [%]
Weight       : 129

```

```

1 : MSSIEPKVMM VGANKKQRTV QASSRKGCMR GKGGPDNASC TYKGVQRQRTW GKWVAEIREP
   * * *      **      ** *      * * *      * * *      * * *
1 : M---EKSSSM -----KQ--- ---WKKGPAP GKGGPQNALC QYRGVQRQRTW GKWVAEIREP

61 : NRGARLWLGT FDTREAAAL YDSAARKLYG PEAHLNLP-- -----ESL-- -----RSYP
   ***** * *   *** *   ** *   ***** *      *****
47 : KKRARLWLGS FATAEEAAMA YDEAALKLYG HDAYLNPLHL QRNTRPSLSN SQRFKWVPSR

106 : KTASSPAS-- ----QTPS- ----- SNTGGKS--- SSDSESPCS- -----SNEMS
   * * *      **      * * *      * * *      * * *
107 : KFISMFPPSCG MLNVNAQPSV HIIQQRLEEL KKTGLLSQSY SSSSSSTESK TNSFLDEKT

140 : -----SC G-----R VTEEISWEHI NVDPVMDSD SIWE----- ----EATMSL
   *      *      *      *      *      *      *      *
167 : SKGETDNMFE GGDQKKPEID LTFELQQLGI LKDENEAEPs EVAECHSPPP WNEQEETGSP

174 : GFPWVHEGDN DI----- -SRFDTCSG GY----- -SNWDSFHSP L
   * *      *      *      *      *      *      *
227 : FRTENFSWDT LIEMPRSETT TMQFDSSNFG SYDFEDDVSF PSIWDDYGS L D

```

+++++

Fig. 5-15

0056504

Sequence 1 : DREB2D.aa
Size : 206
Matching Position : 1 - 206

Sequence 2 : DREB2G.aa
Size : 306
Matching Position : 1 - 306

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 32.08 [%]
Weight : 144

```

1 : MSSIEPKVMM VGANKKQRTV QASSRKGCMR GKGGPDNASC TYKGVQRQTW GKWVAEIREP
    *          **          ***** ***** ** * * ***** *****
1 : EEEQPP-----AKK--RN MGRSRKGCMK GKGGPENATC TFRGVQRQTW GKWVAEIREP

61 : NRGARLWLGT FDTSEAAALA YDSAARKLYG PEHLN-----
    *** ***** * ** * ** * ** * ** * ** * **
52 : NRGTRLWLGT FNTSVEAAMA YDEAAKLYG HEAKLNLVHP QQQQVVVNR NLSFSGHGSG

98 : ----- PESLRSYPKT AS-SPASQTT PSS-----NTGGKSS -----
    *          ** * * **          *          **
112 : SWAYNKKLDM VHGLDLGLGQ ASCSRGSCSE RSSFLQEDDD HSHNRCSSSS GSNLCWLLPK

127 : -SDS-----ES PCSS-----NEMS-----S CGRVTEEISW
    ***          *          *          * **          *          *
172 : QSDSQDQETV NATTSYGGEG GGGSTLTFST NLKPKNLMSQ NYGLYNGAWS RFLVGQEKKT

151 : EHINVDLPVM DDSSIWEE--ATMSLGFPPV H-----EGD-----N DISRFDTGIS
    ** *          ** *          *          *          *          *
232 : EH---DVSSS CGSSDNKESM LVPSCGGERM HRPELEERTG YLEMDDLLEI DDLGLLIGKN

194 : GGYSNW--DS FHSP---L
    * **          *
289 : GDFKNWCCEE FQHPWNWF

```

+++++

Sequence 1 : DREB2D.aa
Size : 206
Matching Position : 1 - 206

Sequence 2 : DREB2H.aa
Size : 177
Matching Position : 1 - 177

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 32.03 [%]
Weight : 101

```

1 : M-----SSIEPK-----VMMVGANKK QR-TVQASSR KGCMRGKGGP
    *          * *          * *          * ** *****
1 : MPRKRKSRGT RDVAEILRKW REYNEQTEAD SCIDGGGSKP IRKAPPKRSR KGCMKGKGGP

```

Fig. 5-16

0056504

```

36 : DNASCTYKGV RQRTWGWVA EIREPNRGAR LWLGTFTSR EAALAYDSAA RKLYGPEAHL
    * * * * *
61 : ENGICDYTG V RQRTWGWVA EIREPGRGAK LWLGTFSY EAALAYDEAS KAIYGQSARL

-96 : NLPESLRSYP KTASSPASQT TPSSNTGGKS SSDSESPCSS NEMSSCGRVT EEISWEHINV
    **      *      *      *      *
121 : NL-----P LLPLCQARLL HFLMN--LKF VHVRIQMQL VLVRS---LT SRIS-----

156 : DLPVMDSS I WEEATMSLGF PWVHEGDNDI SRFDTGISGG YSNWDSFHSP L
    * *      *      *
163 : ----KMLSPI --TALVKLG- -----R Y

```

+++++

```

Sequence 1      : DREB2E.aa
Size            : 244
Matching Position : 1 - 244

```

```

Sequence 2      : DREB2F.aa
Size            : 277
Matching Position : 1 - 277

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
* N+            : 2

Matching         : 27.52 [%]
Weight          : 173

```

```

1 : MEKEDNGSKQ SSSASVVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGC MRGK
    ***      ***
1 : MEK-----SSS-----MK QWKKGPAR GK

61 : GGPENPVCRF RGVRQRVWGK WVAEIREPVS HRGANSSRSK RLWLGT FATA AEAALAYDRA
    *** * * * *
19 : GGPQNALCQY RGVRQRTW GK WVAEIREP-- ----KKRA RLWLGSFATA EEAAMAYDEA

121 : ASVMYGPYAR LN-----FP-----
    * ** * **
71 : ALKLYGHDAY LNLPHLQRNT RPSLSNSQRF KWPVSRKFIS MFPSCGMLNV NAQPSVHI IQ

135 : ----EDLGGG RKKDEEAESS GGYWLETN-- ----KAGN GVIETEGG-- -KDYVVY NED
    * *      **      **
131 : QRLEELKKTG LLSQSYSSSS SSTESKTNTS FLDEKTSKGE TDNMFEGGDQ KKPEIDLTEF

180 : AIELGHDKTQ N---PMTDNE --IVNPAVKS EEGYSYDR-F KLDNGLLYNE PQS-----
    ** * * * *
191 : LQQLGILKDE NEAEPSEVAE CHSPPPWNEQ EETGSPFRTE NFSWDTLIEM PRSETTTMQF

227 : -SSYHQGGGF --DSYF---- --EYFRF
    **      *
251 : DSSNFGSYDF EDDVSFPSIW DYYGSLD

```

+++++

```

Sequence 1      : DREB2E.aa
Size            : 244

```

Fig. 5-17

0056504

Matching Position : 1 - 244
Sequence 2 : DREB2G.aa
Size : 306
Matching Position : 1 - 306

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2
Matching : 25.07 [%]
Weight : 197

```

1 : MEKEDNGSKQ SSSASVVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGCMRGK
1 : ----- ** * * **** **
1 : -----EEE QPPAKKRNMG RSRKGCMKGK

61 : GGPENPVCRF RGVQRVWGK WVAEIREPVS HRGANSSRSK RLWLGTfATA AEAALAYDRA
**** * * ***** ** ***** * **** *
24 : GGPENATCTF RGVQRWTGK WVAEIREP-- -----NRGT RLWLGTfNTS VEAAMAYDEA

121 : ASVMYGPYAR LN----- -----FPE DLGG-----
* ** * ** *** *
76 : AKKLYGHEAK LNLVHPQQQ QVVVNRNLSF SGHSGSGSWAY NKKLDMVHGL DLGLGQASCS

141 : RKKDEEAES- -----SGG YWL-----ETNKA--GNGV
* * * * ** ** *
136 : RGSCSERSSF LQEDDDHSHN RCSSSSGSNL CWLLPKQSDS QDQETVNATT SYGGEGGGGS

165 : IET-----EGGKDYVV YN-----EDAIELGHDK TQNPMTDNEI VNPAVKSEEG
* * ** ** *
196 : TLTFSTNLKP KNLMSQNYGL YNGAWSRFLV GQEKTEHDV SSSCGSSDNK ESMLVPSCGG

208 : YSYDRFKL-- -----DNG LLYNEPQSSS YHQGGGFDSY FEYF-----R F
* * * * *
256 : ERMHRPELEE RTGYLEMDDL LEIDDLGLLI GKNGDFKNWC CEEFQHPWNW F

```

+++++

Sequence 1 : DREB2E.aa
Size : 244
Matching Position : 1 - 244

Sequence 2 : DREB2H.aa
Size : 177
Matching Position : 1 - 177

Matching Condition:

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2
Matching : 29.92 [%]
Weight : 114

```

1 : MEKEDNGSKQ SSSASVVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGCMRGK
* * * * *
1 : MPRKRKSRGT RDVA--EILR KWREYNEQTE A-DSCIDGGG SKPIRKAPPK RSRKGCMKGK

```

Fig. 5-18

```

                                -0056504
61 : GGPENPVCRF RGVQRVWVK WVAEIREPVS HRGANSSRSK RLWLGTFFATA AEAALAYDRA
    ***** * ***** ** ***** ** ***** ***** *
58 : GGPENGICDY TGVQRQWVK WVAEIREP-- GRGA----- KLWLGTFFSS YEAALAYDEA

121 : ASVMYGPYAR LNFPELGGG RKKDEEAESS GGYWLETNKA GNGVIETEGG KDYVVYNEDA
    ** ** ** * * * * *
110 : SKAIYQGSAR LNLP-LLPLC QAR----- ---LLHFLMN LKFVHVRIQM QDLV-----

181 : IELGHDKTQN PMTDNEIVNP AVKSEEGYSY DRFKLDNGLL YNEPQSSSYH QGGGFDSYFE
    * * * *
153 : --LVRSLTSR ISKMLSPITA LVK----- -----

241 : YFRF
    *
174 : LGRY

```

+++++

```

Sequence 1      : DREB2F.aa
Size            : 277
Matching Position : 1 - 277

Sequence 2      : DREB2G.aa
Size            : 306
Matching Position : 1 - 306

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*Nt          : 2

Matching     : 31.41 [%]
Weight       : 138

```

```

1 : ME-----KSS SMKQWKKGPA RGKGGPQNAL CQYRGVRQRT WGWVVAEIRE PKKRARLWLG
    * * * * ***** * ***** ***** *
1 : EEEQPPAKKR NMGRSRKGCN KGKGGPENAT CTFRGVRQRT WGWVVAEIRE PNRGTRLWLG

56 : SFATAEEAAM AYDEAALKLY GHDAYLNLPH LQ-----RN TRPSLSNSQR FKWVPSRKFI
    * * ***** ** * * * * * * * *
61 : TFNTSVEAAM AYDEAALKLY GHEAKLNLVH PQQQQVQVVN RNLSFSGHGS GSW-AYNKKL

110 : SMFPSCGMLN VNAQPSVHI QQRLEELKKT GLLSQSYSSS SS-----STE SKTNTSFLDE
    * * * * * * * *
120 : DMVHGLDLGL GQASCSRGSC SERSSFLQED DDHSHNRCSS SSGSNLCWLL PKQSDS-QDQ

165 : KTSKGETDNM FEGG----- --DQKKP--- ---EIDLTEF LQLGLILKDE NEAEPSEVAE
    * * * * * *
179 : ETVNATTSYG GEGGGGSTLT FSTNLKPKNL MSQNYGLYNG AWSRFLVGQE KKTEDHVSSS

211 : CHS--PPPWN EQEETGS--P FRTENFSWDT LIEM-PRSET TTMQFDSSNF GSYDFEDDVS
    * * * * * *
239 : CGSSDNKESM LVPSCGGERM HRPELEERTG YLEMDDLLEI DDLGLLIGKN GDFKNWCCEE

266 : FPSIWDYYGS LD
    * *
299 : FQHPW----N WF

```

+++++

Fig. 5-19

0056504

Sequence 1 : DREB2F.aa
Size : 277
Matching Position : 1 - 277

Sequence 2 : DREB2H.aa
Size : 177
Matching Position : 1 - 177

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 21.52 [%]
Weight : 192

```

1 : M---EKS--- -----SSMKQWK KGPARGKGGP
   *  **
1 : MPRKRKSRGT RDVAEILRKW. REYNEQTEAD SCIDGGGSKP IRKAPPKRSR KGCMKGKGGP

22 : QNALCQYRGV RQRTWGWVA EIREPKKRAR LWLGSFATAE EAAMAYDEAA LKLYGHDAYL
    * * * * *
61 : ENGICDYTGV RQRTWGWVA EIREPGRGAK LWLGTFSSTY EAALAYDEAS KAIYQGSARL

82 : NLPHLQRNTR PSLNSQRFK WVPSRKFISM FPSCGMLNVN AQPSVHIQQ RLEELKKTGL
    *** * * * *
121 : NLPLLPLCQA RLLHFLMNLK FV-----HVRIQMQ DL-----V

142 : LSQSYSSSSS STESKTNTSF LDEKTSKGET DNMFEQGDQK KPEIDLTEFL QQLGILKDEN
    * * * * *
153 : LVRSLTSRIS KMLS-----PITAL VKLG-----

202 : EAEPSEVAEC HSPPPWNEQE ETGSPFRTEN FSWDTLIEMP RSETTTMQFD SSNFGSYDFE
176 : -----

262 : DDVSFPSIWD YGSLD
176 : -----RY
  
```

+++++

Sequence 1 : DREB2G.aa
Size : 306
Matching Position : 1 - 306

Sequence 2 : DREB2H.aa
Size : 177
Matching Position : 1 - 177

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 24.41 [%]
Weight : 192

Fig. 5-20

```

                                -0056504
1 : ----- --EEEQ---- -----PP AKKRNMGSR KGCМКGКGGP
      ** * * * *
1 : MPRKRSRG RDVAEILRKW REYNEQTEAD SCIDGGGSKP IRKAPPKRSR KGCМКGКGGP

27 : ENATCTFRGV RQRTWGKWVA EIREPNRGTR LWLGTFTSV EAAMAYDEAA KKLYGHEAKL
      ** * * * *
61 : ENGICDYTG RQRTWGKWVA EIREPGRGAK LWLGTFSY EAALAYDEAS KAIYQQSARL

87 : NLVHPQQQQ VVVRNLSFS GHGSGSWAYN KKLDMVHGLD LGLGQASCSR GSCSERSSFL
      ** * * *
121 : NL----- -----PL LPLCQA-----

147 : QEDDDHSHNR CSSSSGSNLC WLLPKQSDSQ DQETVNATTS YGGEGGGGST LTFSTNLKPK
      * * *
131 : -----RL LHFLMNLKFV

207 : NLMSQNYGLY NGAWSRFLVG QEKKTEHDVS SSCGSSDNKE SMLVPSCGGE RMHRPELEER
      * * * *
143 : HVRIQMQL- -----VLV- -----RSLTSRISK- -MLSP-----

267 : TGYLEMDDL EDDLGLLIG KNGDFKNWCC EEFQHPWNWF
      * * *
168 : ----- -ITALVKL-- -----GRY

```

Fig. 6

DREB1C.nuc 1:ATGAACCTATTTT...CTGCCTTTTCTGAAATGTTT...GGCTCCGATTACGAGTCTCCGCTTTCCTCAGGCGGTGATTACA
DREB1D.nuc 1:ATGAATCATTTTTACTCTACATTCCGAGACTCGTTTCTCTCAATCTCCGATCATAGATCTCCGCTTTCAGACAGTAGTGAGTGT
DREB1A.nuc 1:ATGAACCTATTTT...CTGCCTTTTCTGAAATGTTT...GGCTCCGATTACGAGTCTCCGCTTTCCTCAGGCGGTGATTATA
DREB1B.nuc 1:ATGAACCTATTTT...CAGCTTTTCTGAAATGTTT...GGCTCCGATTACGAGCTC...ATGGAAACCGACG
DREB1E.nuc 1:.....ATGGCGGACATTATT
DREB1F.nuc 1:.....ATGAATAATGATG

DREB1C.nuc 77:GTCCGAAGCTTGCCACGAGCTGCCCCAAGAAACAGCGGGAAAGGAAGAAGTTTCGTGAGACTCGTCACCCCAATTTACAGAGGAGT
DREB1D.nuc 86:CACCAAGAGTTAGCTTCAAGTTCTCCAAAGAAACGAGCTGGGAGGAAGAAGTTTCGTGAGACACGTCATCCGATTACAGAGGAGT
DREB1A.nuc 77:TTCCGACGCTTGCCGAGCAGCTGCCCCAAGAAACAGCGGGGTCTTAAGAAGTTTCGTGAGACTCGTCACCCCAATTTACAGAGGAGT
DREB1B.nuc 68:GTCCGACGTTGGCCACGAGTTCTCCGAAGAAACAGCGGGGCCGTAAGAAGTTTCGTGAGACTCGTCACCCCAATTTACAGAGGAGT
DREB1E.nuc 14:ATATCACCGTGGCGGAGATGAACCAAGAAGCGTGCCTGCACGAGGATTTTCAAGGAGACACGTCACCCCAATTTACAGAGGCGT
DREB1F.nuc 14:ATATTATTCTGGCCGAGATGAGGCCTAAGAAGCGTGCGGGAAAGGAGAGTGTTTAAGGAGACACGTCACCCCAATTTACAGAGGCGT

DREB1C.nuc 162:TCGTCAAAGAACTCCGGTAACTGGGTGTGTGAGTTGAGAGAGCCAAACAAGAAACGAGGATTGGCTCGGGACTTTCCAAACC
DREB1D.nuc 171:TCGTCAGAGGAATTCCTGGTAAATGGCTTTTCTGAAGTTAGACAGCCCTAATAAGAAATCTAGGATTGGTTGGGTACTTTTCCGACG
DREB1A.nuc 162:TCGTCGAGCAAACTCCGGTAACTGGGTTTTGTGAGTTAGAGAACCCAAACAAGAAACAGGATTGGCTCGGAACTTTCCAAACC
DREB1B.nuc 153:TCGTCAAAGAACTCCGGTAACTGGGTTTTCTGAAGTTGAGAGAGCCAAACAAGAAACAGGATTGGCTCGGGACTTTCCAAACC
DREB1E.nuc 99:GCGGCGTAGGGACGGCGCAAAATGGGTATCGGAAGTCCGTGAACCGATTTCATCAGCGTCSAGTCTGGCTCGGAACTTTCCGACG
DREB1F.nuc 99:AAAGCGGAGGAACGGTGACAAATGGGTCTCGCAAGTCAGAGAACCCAGCGCACCAACCGCCGCTTTGGCTCGGGACTTTATCCACA

DREB1C.nuc 247:GCTGAGATGGCAGCTCGTGCTCAGCAGCTGCCGCCATAGCTCTCGTGGCAGATCTGCCGTGTCTCAATTTCCGCTGACTCGGCTT
DREB1D.nuc 256:GTTGAAATGGCTGCTCGTGCTCATGATGTTGCTGCTTAGCTCTCGTGGTCCCTCTGCTGTGTCTCAATTTCCGCTGATCTGCTT
DREB1A.nuc 247:GCTGAGATGGCAGCTCGAGCTCAGCAGCTGCGCTTAGCCCTTCGTGGCCGATCAGCGTGTCTCAATTTCCGCTGACTCGGCTT
DREB1B.nuc 238:GCTGAGATGGCAGCTCGTGCTCAGCAGCTGCTGCTTAGCCCTTCGTGGCCGATCAGCATGTCTCAATTTCCGCTGACTCGGCTT
DREB1E.nuc 184:GCAGATATGGCCGCACTGCTCAGCAGCTGCGGCTTCTTGGCTCTGCGCGGAGATCCGCGTGTGTTGAATTTCTCGGATCTGCTT
DREB1F.nuc 184:GCAGATATGGCAGCGCGTGCTCAGCAGCTGCGGCTTCTTGGCTCTGCGCGGAGATCCGCGTGTGTTGAATTTCTCGGATCTGCTT

DREB1C.nuc 332:GGCGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGCTGAAGCCCGTTGAATTTTCAA...GATGAG
DREB1D.nuc 341:GGCGGCTTCGTATTCCTGAGACTACTTCTCTAAGGAGATTCAGAAAGCTGCGTCTGAAGCTGCAATGGCGTTTCA...AATGAG
DREB1A.nuc 332:GGCGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAGATCCAAAGCGCGCGGCTGAAGCTGCAATGGCGTTTCA...GATGAG
DREB1B.nuc 323:GGCGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAGATCCAAAGCGCGGCTGCTGAAGCGCGGTTGGCTTTTCAA...GATGAG
DREB1E.nuc 269:GGAGGTTGCGGTTGCCGGCATCCACTGATCCGACACGATCAGGACGATCAGGCGGAGATGTTTCAAGCCCGGAG
DREB1F.nuc 269:GGCGGCTTCGGTGCCGGAATCCAAATGATCCGGATGTGATAAGAGAGTTCGGCGGAGAGCTGCGGAGATGTTTAGCCCGGTGGA

DREB1C.nuc 415:AT.....GTGTCTATGACCAAGGATGCTCATGGTCTTGACATGGAGGA...GACCTTGGTGGAGGCT...ATTTATA
DREB1D.nuc 424:ACTACGACGGAGGGATCTAAAACTGCGCGGAGGCGAGGAGGCGGCGAGGAGGG...GGTGAAGGAGGGGGAG...AGGAGGG
DREB1A.nuc 415:AT.....GTGTGATGCGGACCAAGGAT...CATGGCTTCGACATGGAGGA...GACGTTGGTGGAGGCT...ATTTATA
DREB1B.nuc 406:AC.....GTGTGATGACGACCAAGGATCATGGCTTCGACATGGAGGA...GACGTTGGTGGAGGCT...ATTTATA
DREB1E.nuc 354:GTTT.....AGTACAGGAATTACCGTTTTTACCTCAGCCAGTCA...TTTGACAG...
DREB1F.nuc 354:TTTA.....GAAGTCAATTACCGTTTTTCTTGTGCGGGAATGATGTGGATTGEGTTTGGTTTCCGGCTCTG

DREB1C.nuc 482:CGCGGAAC...AGAGCCAAGATGCGTTTTATATGGATGAAGAGGCGATGTTGGGGATGCTAGTTTGGTGGATAACATGGCG
DREB1D.nuc 503:CGGAGGAGC...AGAATGGTGGTGTGTTTTATATGGATGATGAGGCGCTTTTGGGGATGCCAAGCTTTTTTGAAGATATGGCG
DREB1A.nuc 479:CGGCGGAAC...AGAGGCAAAATGCGTTTTATATGACGATGAGGCGATGTTGAGATGCCGAGTTTGGTGGTAATATGGCG
DREB1B.nuc 473:CACCGGAAC...AGAGCCAAGGTCGTTTTATATGGATGAGGAGACATGTTTGGGATGCCGACTTTGTTGGATAATATGGCTG
DREB1E.nuc 402:..TCGG.....ATGAAGGAGTCCGTGGAATGATGATGAGGCTCGCGG
DREB1F.nuc 431:GTTCCGGATCCGAGGAGAGGAATCTTCTTCGTTATGGATTGAGACTACGAAGAAGTCTCAACGACCATGATGAGACTCGCGG

DREB1C.nuc 563:AGCGGATGCTTTTACCGTCCGC...GTGCGTTCAATGGAATCATAATT...TTGATGTCGAGGGAGA...TGATGA
DREB1D.nuc 584:AGGGGATGCTTTTGGCCGCGCC...CGAAGTTGGCTGGAATCATAAC...GACTTTGACGGAGT...GGTGA
DREB1A.nuc 560:AGGGGATGCTTTTGGCCGCTTCC...GTCCGTACAGTGGAAATCATAATC...ATGAAGTCGACCGGCA...TGATGA
DREB1B.nuc 554:AGGGCATGCTTTTACCGCGGCC...GTCTGTTCAATGGAATCATAATT...ATGACGCCAAGGAGA...TGCTGA
DREB1E.nuc 443:AGGAGCGGTGATGTCGCCGCCAAGCATCGTACATGA...TATGAAT...ACGAGTGTGTACGTTGGACGAGAAATGTGTACGA
DREB1F.nuc 515:AGGGGCCACTAATGTGCGCGCGCGCATCGTATGAGAGCATGACTCTACTAATGTTTACACGGAAGAAGATGTGTATGA

DREB1C.nuc 630:CG...TGTCCTTATGGAGCTATTAA.....
DREB1D.nuc 648:CG...TGTCACCTCTGAGCTTTTGACGAGTAA
DREB1A.nuc 627:CGACGATCTGTTATGGAGTTATTAA.....
DREB1B.nuc 621:CG...TGTCGCTTTGGAGTTACTAA.....
DREB1E.nuc 522:AGATTGTCACCTTGGAGTTACTAA.....
DREB1F.nuc 600:AGATATGTCATTGTTGGAGTTACAGATATTAA

Fig. 7-1

[illegible]

Fig. 7-2

[illegible]

Fig. 8

```

DREB1A 1: ...MNSFSAFSEMFSGSDYESSVSSGGDYIPTLASSCPKKPAGKKKPRETRHPPIYRGVRR
DREB1B 1: ...MNSFSAFSEMFSGSDYEP...QGGDYCEPLATSCPKKAGKKKPRETRHPPIYRGVRR
DREB1C 1: ...MNSFSAFSEMFSGSDYESSVSSGGDYSPKLATSCPKKAGKKKPRETRHPPIYRGVRR
DREB1D 1: MNPFTSTPPDSFLSISDMRSPVSDSSECSPLASSCPKKPAGKKKPRETRHPPIYRGVRR
DREB1E 1: .....MENDDITVEMKPKKAGRIIFKMETRHPPIYRGVRR
DREB1F 1: .....NNDDITLAE MRPKKRAGRVKSKETRHPPIYRGVRR

DREB1A 57: RNSGKNVCEVREPNKKTRINLGTFTAE MAARAHDVAALALRGSAACLNFAADSANRLRI
DREB1B 54: RNSGKNVCEVREPNKKTRINLGTFTAE MAARAHDVAALALRGSAACLNFAADSANRLRI
DREB1C 57: RNSGKNVCEVREPNKKTRINLGTFTAE MAARAHDVAALALRGSAACLNFAADSANRLRI
DREB1D 60: RNSGKNVCEVREPNKKSRIINLGTFTVEMARAHDVAALALRGSAACLNFAADSANRLRI
DREB1E 36: RQDKNVCEVREPEQRRVILGTPTADMAARAHDVAALALRGSAACLNFSDSANRLPV
DREB1F 36: RQDKNVCEVREPEQRRVILGTPTADMAARAHDVAALALRGSAACLNFAADSANRLPV

DREB1A 116: PESTCAKDIOKAAREAAALAFODEMCDATTDHG.PDNEETLVEAIYTAE.....QSENAF
DREB1B 113: PESTCAKDIOKAAREAAALAFODECTTTTNEGLDNEETMVEAIYTP.....QSECAF
DREB1C 116: PESTCAKEIOKAAREAAALNFODEMCHMTTDAEGLDNEETLVEAIYTP.....QSDAF
DREB1D 119: PETCPKSIOKAAREAAALAFONETTEGSKTA.AEAEEAAGCGVREGERRAEENGGVF
DREB1E 95: PASTDPDTIRRTAAREAAEMFRPFSTGITVLPASAEFDTSE.....
DREB1F 95: PESNDPDPVIRRVAAEAENFRPVDLESGITVLPACAGDDVDLGFSGSGSGSGSEERNSS

DREB1A 169: VMHDEAMFEMPSLLANNAEGMLLPSPVQRRNH.....EVDGDDDDVSLNSY..
DREB1B 167: VMDEETMFGMPTLLDNNAEGMLLPSPVQRRNY.....DGECDGD.VSLNSY..
DREB1C 170: VMDEBAMLGHSLLDNNAEGMLLPSPVQRRNYF.....DVEGDDDD.VSLNSY..
DREB1D 177: VMDDGALLGMPNPFENNAEGMLLPPEVQRRHN.....DFDGVGD.VSLNSFDE
DREB1E 135: .....DEGVAGMMKRLAEPLMSRPSYIDMN..TSVYVDEEMCYEDLSLSY..
DREB1F 154: SYGFGDYEEVSTTMMRLAEGPLMSRPSYMEDMTNTNVTYTEEMCYEDMSLSYRY

```

Fig. 9

DREB2A	1:AAVYDQSGDRNRTOIDTSRKRSRSGDGTVAERLKRWKKEYNEIVTEVSTK.....KRVPAKSGKKGCNKKGKGG
DREB2B	1:AAVVEQTG.....TEQPKRKSRARAGGLTVADRLLKKWKKEYNEIVEASAVKEG..EKPKRKVPKAGSKKGCKNKKGKGG
DREB2C	1:MPSE.....IVDRKRKSR...GTRDVAEILRQWREYNEQIEAESCIDGGPKSIRKPPPKGSRKKGCKNKKGKGG
DREB2D	1:.....NSSIEPKVMVGANKKQRTVQASSRKKGCKNKKGKGG
DREB2E	1:.....MEKEDNGSKQSSSASVVSRRRRRVVEATLQWEEEGCLARARVQAKGSKKGCKNKKGKGG
DREB2F	1:.....MEKSSSMKQ.....WKKGPARKGKGG
DREB2G	1:.....MEEQPPAKKRNMGSRKKGCKNKKGKGG
DREB2H	1:MP.....RKRSR...GTRDVAEILRQWREYNEQIEAESCIDGGGSKPIRKAPPKRSRKGCNKKGKGG

DREB2A	72:PENSRCSTFRGVRQRIINGKKNVAEIREPN.....RGSRLNLGTFPTAQEAASAXDEAAKAMVGP LARLNPFRSD...
DREB2B	71:PDNSHCSTFRGVRQRIINGKKNVAEIREPK.....IGTRLNLGTFPTAEKAAAYDEAAATAMVGS LARLNPQSV...
DREB2C	65:PENGICDYRGVRQRIINGKKNVAEIREPD.....GGARLNLGTFSSSYEAALAYDEAAKAIYQ SARLNLPEITNRS
DREB2D	35:PDNASC TYKGVRORTWGNVAEIREPN.....RGARLNLGTFDTSREAAAYDAAARKLYGPBAHLNLPESLR...
DREB2E	63:PNPVCRTFRGVRQRIINGKKNVAEIREPN.....SHRGANSR...SRKRLNLGTFPTAEAAALAYDRAASVMGPYARLNPEDLG...
DREB2F	21:PNALCQYRGVRQRIINGKKNVAEIREPK.....KRRLNLGTFPTAEAAALAYDEAAL KLYGHDATLNLPHIQRN.
DREB2G	27:PNATCTFRGVRQRIINGKKNVAEIREPN.....RGTRLNLGTFPTSVAAAMAYDEAAKLYGHEAXLNLVHPQQQ...
DREB2H	60:PENGICDYTGVRQRTWGNVAEIREPG.....RGAKLNLGTFSSSYEAALAYDEASKALYQ SARLNLPLLP...

DREB2A	138:.....ASEVTSTSSQSEVCTVETPGCVK....UKTEPDCEKSPFSG..GVPEMYCLEN.....GAEMKRGV
DREB2B	137:.....GSEFTSTSSQSEVCTVENKAVDGVCKVKEHEDTDCESNPFQILDVREESCGRTRPDSCTVGHQDMNSSL
DREB2C	135:SSTAATAATVSGSVTAFSDSEVCAREDTNASSGFGQVKLEDCSDXYLLDSSQCIKEELKKEE....VREHNLA V
DREB2D	102:.....SYPKTASSPASQTTPS.....
DREB2E	138:.....GGRKHDEEAESSGGYWLKTNKAGNGVETFG....GKDYVYVN.....
DREB2F	89:.....TRPSLSNSQRFKXWVPSR....KPFISMFPSCGMLNVAQPSVHIQQRLBELKKTGL
DREB2G	95:.....QQVVNRNLFSGCHGSGSWAYNKKLDVHGLDLGLGQASC SRGSCSERSSFLQEDDD
DREB2H	126:.....LQCARLLHFLMNLKFWHVRIQMQLVLVS.....LTSR.....

DREB2A	196:KADKXNLSEFEHNYWSDILKEKX...QKEQGIVETCQQQQQ...DSISVADYGP..NDV..DQSHLDS....SDM
DREB2B	207:NYD..LLEFEQYWGQVLQEKEXPKQEEIEIQQQQEQQQQQLQPDLLTVADYGPWSNDIVNDQTSWDP....NEC
DREB2C	208:GFG....IGQDSKRETLDAWLMGNENQEPLEFGVDETFD..INELGILNDNNVSGQIETMQYQVDRHPNFSYQTQ
DREB2D	118:..SNTGCKSSDS.....ESPCSS...NEMSSCG.....RVTEEISWEHINVDLPVMD.....S
DREB2E	177:.....EDAIELGHDKTQNPMTDNEIVNPAVKSEEG
DREB2F	142:LSQSYSSSSST.....ESXTNTSFLDEKTSKGETDNMFEGDQXKPEIDLTEFLQQLGILKDN.....SA
DREB2G	153:HSHNRCSSSSGSNLCWLLPKQSDSQDQETVNATTSYGOEGGGSTLTFTSNLKPKNLNSQNYGLYNGAWSRPLVGQEK
DREB2H	160:.....ISKMTSPI.....TALVKLGRY.....

DREB2A	259:FDVDELLRDINGDDVFAGLNQDRYPGNVANGSYRPESQSQGPDPLQSLNYGIPPFQLEGKXGNGFFDPLSYLDLEN
DREB2B	279:FDINELLGDLN.....EPGPHQSQDQ...NHVNSGSDYDLHPLHLEPHDG.HEFNGLSSLDI..
DREB2C	278:FPNSNLLGSFN.....PMETAPQGVQDYGCPYVQPSDMENYGDLDHRRHRLDLDIQDLDFGDKDVHGST...
DREB2D	164:SIWBEATMSLGPFWVHEGDN.....DISR.....FDTGISGGY.....SNWDGFSH SPL...
DREB2E	208:YSYDRFK.....LDNGLLYNEPQSSSYHQGGGDFSYPEYFRF.....
DREB2F	204:EPSEVAECHSPPPWNEQETGSPFTENFSWDTLIEMPRSETTMQFDSSNFGSYDFEDDDVSFPSIWYIGSLD...
DREB2G	231:KTEHDVSSSCGSSDNKESMLVPSCGGERMHRPELEERTGYLEMDDLLEIDDLGLLIGKNGDFXNWCCEFOHPWNF
DREB2H	:

Fig. 10



strain 9



strain 10



non-transformant

Fig. 11

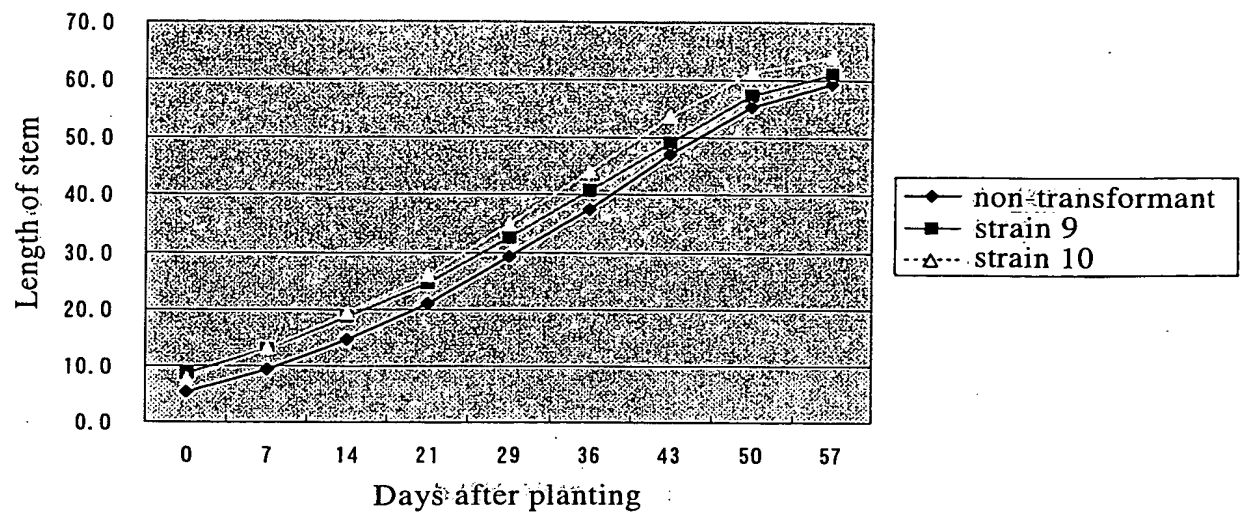
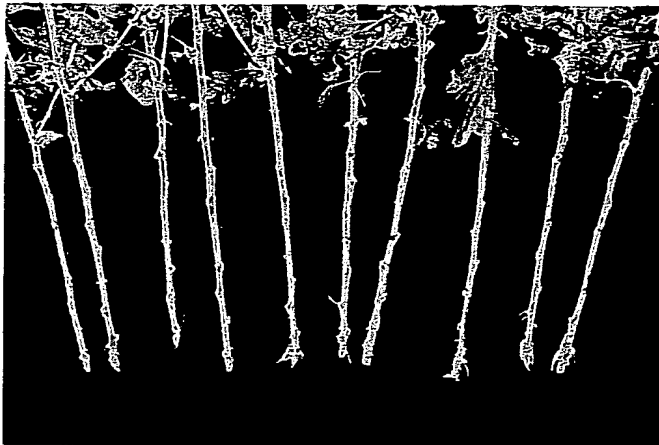


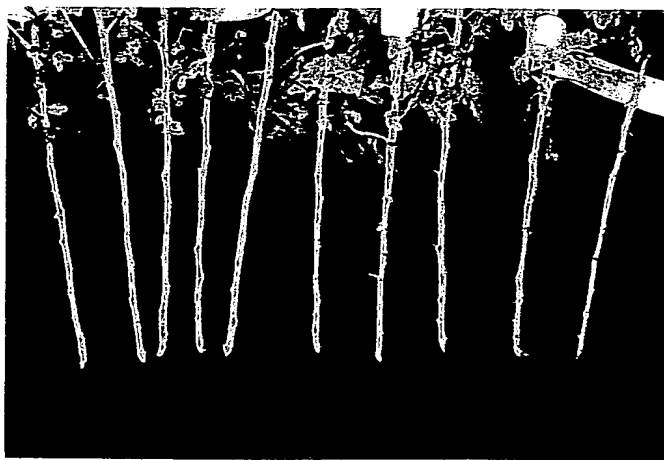
Fig. 12



strain 9



strain 10



non-transformant